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GenCore version 5.1.6
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Title: 10.5-93-9-53A-74 Sequence: 1183, 582-54C
US-09-939-853A-74 able: US-09-939-853A-74 lagctagagctccaaggaccctctctttggatgatgcctag 118 able: LDENTITY NUC dapop 10.0 , Gapext 1.0 3470272 seqs, 21671516995 residues ber of hits satisfying chosen parameters: 6940544 B seq langth: 00000000 sesing: Minimum Match 0% Listing first 45 summaries GenEBMl: * GenEBMl: * GenEBMl: * 1 gb ba: * 2 gb_htg: * 4 gb_or: * 5 gb_pl: * 8 gb_pl: * 11 gb px: * 12 gb_pl: * 13 gb_ln: * 13 gb_ln: * 14 gb_or: * 15 em_hu: * 16 em_hu: * 17 gb_pl: * 18 em_hu: * 19 em_hu: * 22 em_hu: * 23 em_htg: hu: * 24 em_bi: * 25 em_htg: hu: * 26 em_to: * 27 em_htg: hu: * 28 em_htg: hu: * 29 em_htg: hu: * 21 em_htg: hu: * 22 em_htg: hu: * 23 em_htg: hu: * 24 em_htg: hu: * 25 em_htg: hu: * 26 em_htg: hu: * 27 em_htg: hu: * 28 em_htg: hu: * 29 em_htg: hu: * 20 em_htg: hu: * 21 em_htg: hu: * 22 em_htg: hu: * 23 em_htg: hu: * 24 em_htg: hu: * 25 em_htg: hu: * 26 em_htg: hu: * 27 em_htg: hu: * 28 em_htg: hu: * 29 em_htg: hu: * 20 em_htg: hu: * 20 em_htg: hu: * 21 em_htg: hu: * 22 em_htg: hu: * 23 em_htg: hu: * 24 em_htg: em_htg: hu: * 24 em_htg: em_htg: hu: * 25 em_htg: hu: * 26 em_htg: hu: * 27 em_htg: em_htg: hu: * 28 em_htg: hu: * 29 em_htg: hu: * 20 em_htg:
table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Bayon 10.0 , Gapext 1.0 Gensmin Match 100* Listing first 45 summaries Gensmbl:* 1 gb ba:* 2 gb ba:* 2 gb ba:* 3 gb ln:* 4 gb om:* 5 gb om:* 5 gb om:* 6 gb pat:* 11 gb pat:* 12 gb pat:* 13 gb on:* 14 gb ov:* 15 gb on:* 16 gb pat:* 17 gb pat:* 18 gb on:* 19 gb on:* 11 gb sy:* 11 gb sy:* 12 gb on:* 12 gb on:* 13 gb on:* 14 gb ov:* 15 gb on:* 16 em ba:* 17 em bum:* 18 em ln:* 19 em nu:* 22: em on:* 22: em on:* 23: em los:* 24: em los:* 25: em los:* 26: em on:* 27: em sts:* 28: em los:* 29: em ltg on:* 31: em ltg ln:* 32: em ltg on:* 33: em ltg on:* 34: em ltg on:* 35: em ltg on:* 36: em ltg or:* 37: em ltg on:* 38: em ltg or:* 39: em ltg or:* 41: em ltg or
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cessing: Minimum Match 0% Maximum Match 100% Listing first 45 summari GenEmbl:* 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES ## August ##	linear PAT 02-JUL-2002	<pre>Vertebrata; Buteleostomi; ; Hominidae; Homo. Hart,M., Kekuda,R., ., Tomlinson,J.E.,</pre>
* 90	1183 bp DNA from Patent WO0216599. GI:21690555 (human)	nn, Chordata; Craniata; N; Primates; Catarrhini ey,P.B., Grosse,W.M., rek,X.A., Szekeres;E.S ing,R.B.
No. No. No. Sold Section 1183.5.2 1188.38 1188.48 1	AX443133 ON Sequence 74 f. AX443133.1 G. Homo sapiens	Homo sapiens Rukaryota, Mel Mammalia, Buti Burgess, C.E., Shimkets, R.A Topper, J.N. a

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PAT 02-JUL-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proteins and Yang, R.B.
Proteins and Colosse encoding same Patent: WO 0216599-A 76 28-FEB-2002;
Curagen Corporation (US); COR THERAPEUTICS, INC. (US)
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Proteins and nucleic acids encoding same
Patent: WO 0216599-A 74 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS,
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Pred. No. 1.2e-305;
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Matches 1183; Conservative 0
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Cloning and expression of human slap-2: a novel sh2/sh3
domain-containing human slap homologue having immune cell-specific
expression
Patent: WO 0242457-A I 30-MAY-2002;
Patent: WO 0242457-A I 30-MAY-2002;
Pristol-Wyers Squibb Co. (US)
Location/Qualifiers
I. 2567
/ Acganism="Homo sapiens"
// Acganism="Homo sapiens"
// Acganism="Homo sapiens"
// Aby_Expe="Laxon:9606"
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Canag,H., Yang,W.P., Wu,Y., Whitney,G.S., Perez-Villar,J.J. and
Kanner,S.B.
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clone MGC:49845 IMAGE:4429896), complete cds.
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CAGGATCCACTGCCTTGACAATGGCTGCTGTACATCTCACCGGGGCCTCACCTTCCCCTC
                                                             GGAGCCCTGTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTGT
                                                                                                                                                            ACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAA
                                                                                                                              GGAGCCCTGTGTGCTGCAGAGGGCTGGCCGCTCCCTGGCAAGGATATACCCCTACCTGT
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                                                                                                                                                                                                                                                                                1141 CATCAGCCTGAATGACGAGGCTGTCTTTGGATGATGCCTAG 1183
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 3014 from Patent W003039443.
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db xref="taxon:9606"
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DEFINITION
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AUTHORS
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AGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSRE
                                                             KAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYI
                                                                                     SPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWK
ELDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA"
                                                                                                                                   468. .632

// note="SH3; Region: SH3 domain. SH3 (Src homology 3)

// note="SH3; Region: SH3 domain. SH3 (Src homology 3)

// domains are often indicative of a protein involved in

signal transduction related to cytoskeletal organization.

First described in the Src cytoplasmic tyrosine kinase.

// Ab zref="CDD:pfam00018"

// db zref="CDD:pfam00018"

// db zref="SH2; Region: SH2 domain"

// db zref="CDD:pfam00017"
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Matches 1146; Conservative
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                                                             Straubberg, L. C. Feingold, E. A., Grouse, L. H., Derge, J. G., Altschuler, R. D., Collins, F. S., Wagner, L., Schener, C. M., Schuler, G. D., Altschul, S. E., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Baet, N. K., Hopkins, R. F., Jordan, H., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Staplecon, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheefer, C. Raha, S. S., Loquellano, N. A., Peters, G. J., Arameor, R. D., Mullahy, S. J., Bosak, S. A., McEwant, P. J., Manley, K. C., Rale, S. S., Loquellano, N. A., Peters, G. J., Vallalon, D. K., Mallek, J. A., Gunaratne, P. H., Richards, S. W., Vilalon, D. K., Manny, D. M., Sodersten, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, B. X. Scherero, R. J., Mulling, M., Madan, A., Rodrigues, S. Sanchez, A., Mniting, M., Madan, A., Rodrigues, S. Sanchez, A., Mniting, M., Madan, A., Young, A.C., Shevchenko, Y. Butterfield, Y. S., Krzywinski, M. I. Skaiska, U., Sahutz, J., Were, R. Dickson, M. C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Were, R. Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length human and mouse onna Sci. U.S. A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAK Plate: 88 Row: a Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="LocusID: 84174"
'translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTWBAERSKATAVALGSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2538)
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/tissue type="Prostate, adenocarcinoma."
/clone_lib="MIH_MGC_91"
/lab_host="PB10B"
/note="Vector: pCMV-SPORT6"
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/db_xref="GI:27469843"
/db_xref="Tron:cTP"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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us-09-939-853a-74.rge

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Indels
                                                                                                                                                                      Score 825.8; DB 9;
Pred. No. 5.4e-210;
0; Mismatches 2;
   'codon start=1
                                                                                                                                                                          69.8%;
99.8%;
                                                                                                                                                                        Query Match
Best Local Similarity 99.8'
Matches 827; Conservative
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Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo. Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, S. & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CATCCTGGGACCGGATCAGGACACTACAGGATCCACTGCCTTGACATGGCTTGCTGTGACA
                                                                                                                           CGGATGACATCTGCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCC
                                                                              TCTCACCGCGCCTCACCTTCCCCTCACTCCAGGCCCTGGTCGTCGACCATTACTCTGAGCTGG
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                                                        TCTCACCGCGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGG
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Homo sapiens cDNA: FLJ21992 fis, clone HEP06554.
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/note="cloning vector reality"
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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/note="unnamed protein product"
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KEYWORDS
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AUTHORS
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KABELLLLGORNGGAPLIRESGYRRGSYSLSVRLSRPASWBATRHYRTHGLDNGWLYI
KABELLLFPSELQALVORTSSLADDICCLLKEPGYLQRAGPLPGXDIPLPVTVQRTPLNWK
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OY 1118 CTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTGGATGAT 1177 Db 721 CTCCGGAGGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTTGGATGAT 780 Qy 1178 GCCTAG 1183 Db 781 GCCTAG 1183 AX572845 LOCUS AX57284	Mendenhall,M.K., D.G., Mancebo,H Sheng,N. inhibitor of ant sed functional sed cuticals, Inc. (U euticals, Inc. (I euticals, I euti	/db_xref="G1:26004936" /db_xref="G1:26004936" /db_xref="G1:26004936" /db_xref="REMTREMBL:CAD58542" /translation=MGSLPSRRKSLPSELSSSVQGQPVTMEAERSKATAVALG /translation=MGSLPSRRKSLPSELSSSVQGQPVTMEAERSKATAVALG /AGGPAELSLEGEPLTIVSENGDGDWWTVLSEVGGREYNIPSVTHYSHTCLDNGW SPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPL ELDSSLLFSEAATGEESLLSFGLRESLSFYISLNDEAVSLDDA" Duery Match 66.3%; Score 784.4; DB 6; Length 786; Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 398 ATGGGAAGTCTGCCCAAGAAAAATCTCTCCCAAGCTTGAGTTCCTCTGTC 4 398 ATGGGAAGTTCTCCCCAAGAAAAAATCTCTCCCAAGCTTGAGTTCCTCTGTC 4	A STAGGACAGGACCTGTGACCATGGAGAGAGAGCCCAAGCCTTGAGTTCTCTGTCTG
DEFINITION Sequence 4 from Patent W00242452. DEFINITION Sequence 4 from Patent W00242452. AX511153 AX511153 AX511153.1 GI:23392046 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) REPERENCE ORGANISM AUTHORS ACAPLES A4 30-MAY-2002; TITLE AUTHORS ACAPLES A4 30-MAY-2002; The Hospital for Sick Children (CA) ADDATORS LOCATION QUANTIFIES LOCATION ADDATORS AMDIE AMDRES LOCATION ADDATORS AMDIE AMDRES AMDRES AMDRES LOCATION AMDRES AMDRES AMDRES LOCATION ADDATORS AMDRES AMDRES AMDRES AMDRES AMDRES AMDRES AMDRES AMDRES LOCATION ADDATORS AMDRES AMDRES MDRES AMDRES AMDRES AMDRES AMDRES AMDRES AMDRES AMDR	Query Match 66.3%; Score 784.4; DB 6; Length 786; Best Local Similarity 99.9%; Pred. No. 6.9e-199; 1 Indels 0; Gaps 0; QY 398 ATGGGAAGTCTGCCCAGCAGAAGAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTC 457 457 Db 1 ATGGGAAGTCTGCCAGCAGAAGAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTC 60 QY 458 CAAGGCCAGGAACTGTGAACAAGAAGAAGAAGAAGAAGACCAAGCCCAAGCCGTGGCCTG 517 Db 61 CAAGGCCAGGGACCTGTGACCATGGAAGAAGAAGAAGAAGACAAGGCCAACAGCCGTGGCCTG 120 QY 518 GGCAGTTTCCCGGCAGGTGGCCCGAGCTGTCGCTGAGACTGAGCCATTGACC 577 Db 121 GGCAGTTTCCCGGCAGGTGGCCCGGCCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACC 577 Db 121 GGCAGTTTCCCGGCAGGTGGCCCGGCCCGAGCTGTCGCTCGAGACTCGGGGAGCCATTGACC 577	Qy 578 ATCGTCTCTGAGGAGGACTGGAGGACGGTGTCTGAAGTCTCAGGCAGAGATAT 637 Db 181 ATCGTCTCTGAGGACGTGGTGGACGTGTTGTAAGTCTCAGGCAGAGATAT 240 Cy 638 AACATCCCCAGCGTCCACGGGCAACTCTCCATGGGTGATGTATGAGGCTTGAC 697 Db 241 AACATCCCCAGCGTCCACGGCCAAAGTCTCCCATGGGTGTATGAGGGCTTGAGC 697 Cy 698 AAGGAGAAAACCAGAGGAACTGCTATACTCCCATGGGTGTATGAGGGCCTTCCTCATC 350 Cy 758 GGGAAGAACAGAGGAACTGCTGTTACTCTCTGTCAGCCGCCTTCCTCATC 360 Cy 758 GGGAAGAACCAGAAGAGAGGCTCTTACTCTCTGTCAGCCGCCTCAGCCGCCTGCA 817 Db 361 CGGGAAGACCAGAAGAGAGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCTGCA 817 Db 351 CGGGAAGACCAGAAGAGAGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCTGCA 817 Db 361 CGGGAAGACCAGAAGAGACTTTACTCTCTGTCAGTCCGCCTCAGCCCCTGCA 817	0y 121 TCCTGGGACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGCTGACATC 877

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AF326153 786 bp mRNA linear PRI 08-NOV-2001
Homo sapiens Src-like adapter protein-2 mRNA, complete cds.
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Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.
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AGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSRE
KAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYI
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I (bases 1 to 786)
Loreto, M.P. and McGlade, C.J.

Cloning and characterization of human Src-like adaptor protein 2 and a novel splice isoform, SLAP-2-v
Oncogene 22 (2); 266-273 (2003)
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/product="Start=1ike adaptor protein-2"
/product="AAL38197.1"
/protein_id="AAL38197.1"
/db_xref="GI:17351921"
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Loreto, M.P. and McGlade, C.J.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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601 GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGGTG
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Pred. No. 4.7e-166;
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Adapter gene
Patent: WO 0242452-A & 30-MAY-2002,
The Hospital for Sick Children (CA)
Location/Qualiflers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6 from Patent W00242452.
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Best Local Similarity 93.3%;
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Homo sapiens
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KAELLLLLESPENGARDIRESGTRRGSSYSLOVILSRPASWBR RHYRTHCLDNGWLYI
SPRLTFPSLGALVOHYSELADDICCLLKEPCYLQRAGFLPGKDIPLEVTVQRTPLNWK
RLDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein id="AAL29204.î"
db_xref="G1:16797892"
'translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTMBABRSKATAVALGSFP
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to '786)
1 (bases 1 to '786)
1 (bland, S.J., Liao, X.C., Mendenhall, M.K., Zhou, X., Pardo, J., Chu, P., Spencer, C., Fu, A.C., Sheng, N., Yu, P., Pali, B., Nagin, A., Shen, M., Yu, S., Chan, E., Wu, X., Li, C., Woisetschlager, M., Aversa, G., Kolbinger, P., Bennett, M.K., Molineaux, S., Luo, Y., Payan, D.G., Mancebo, H.S.Y. and Wu, J.
Phuctional Cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel Inhibitor of Antigen Receptor Signaling
J. Exp. Med. 194 (9), 1263-1276 (2001)
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Holland, S.J., Mendenhall, M.K., Zhou, X., Spencer, C., Pardo, J.,
Fu, A.C., Sheng, M., Shen, M., Liao, C., Luo, Y., Payan, D.G.,
Mancebo, H.S.Y. and Wu, J.

Direct Submission
Submitted (05-DEC-2000) Rigel Pharmaceutical Inc., 240 East Grand
Avenue, South San Francisco, CA 94080, USA
Location/Qualifiers
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'product="Src-like adapter protein-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
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<u> AGGGAGAAAGCAGAAGTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTTCCTCATC</u>

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ROD 04-NOV-2003
/product="Src-like adaptor protein-2 splice isoform"
| protein id="AAL381981" |
| db xref="d1:17351921" |
| transl ation="MASSEPSRRSIPSPSISSSVQGQBVTMEAERSKATAVALGSFP |
| transl ation="MASSEPSRRSIPSPSISSSVQGQBVTMEAERSKATAVALGSFP |
| AGAPAELSELEDPLIKESCPTRRGSYSLSVRLSRPARMPAKVSHCMLYEGLSRE |
| KARELLILPGRAPGGAFFLIRESCPTRRGSYSLSVRLSRPARMPAKVSHCMLYEGLSRE |
| SPRITFPSLQALVDHYSEGWPAPWQGYTPTCDCAEDTTQLERAGQLPPVF"
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                                                                                                                                                                                                                                         Ouery Match 55.9%; Score 661.8; DB 9; Best Local Similarity 93.3%; Pred. No. 4.7e-166; Matches 734; Conservative 0; Mismatches 2;
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Loreto,M.P. and McGlade,C.J.
Direct Submission
Submited (28-JUL-2000) Brain Tumour Research Centre, Hospital for
Sich Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada
Location/Qualifiers
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1 (bases 1 to 737)

Loreto,M.P. and McGlade,C.J.

Cloning and characterization of human Src-like adaptor protein 2 and a novel splice isoform, SLAP-2-v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACAGCTCCCTCCTGTTTTCTGAAGCTGCCACAGGGAAGAGTCTCTTCTCAGTGAGGTG
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                                                                                                                                                                        CGGGAGAGCCAGAGAGAGAGAGACTCTTACTCTGTCAGTCCGCCTCAGCCGCCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                   TCACCGGGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCG
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="SLAP-2-v"
/codon_start=1
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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817 420 877 480 937 531 997 550 1176

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1117

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AEELLLLPGNPGGAFLTRESQTRRGCYSLSVRLSRPASWDRTRHYRTQRLDNGWLYTS
PRLTFPSLHALVBHYSELADGICCPLREPCVLQKLGPLPGKDTPPPVTVPTSSLNWKK
LDRSLLFLEAPASGEASLLSEGLRESLSSYTSLAEDPLDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MGSLSSRGKTSSPSPSSSGPDQEPVSMQPERRKVTAVALGSFPA
GBQARLSLRLGEPLTIISEDGDWWTVQSEVSGREYHMPSVYVAKVAHGWLYEGLSREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SH3; Region: SH3 domain. SH3 (Src homology 3) domains are often indicative of a protein involved in a signal transduction related to cytoskeletal organisation. First described in the Src cytoplasmic tyrosine kinase. The structure is a partly opened beta barrel" | db xref="CDD:pfam00018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 AGGGCCCCCAAAGCCCTAACCTGTCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCC 333
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                          clone="MGC:60811 IMAGE:30040401"

tissue_type="Hematopoietic Stem Cell,
(iin-/C-Kit+/Sca-1-), mouse, 10 wks"

/clone_lib="NIA Mouse Hematopoietic Stem Cell
(lab_host="DH10B")
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       037. .899
note="SH2; Region: Src homology 2 domains"
db_xref="CDD:cd00173"
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                                                                                                                                                                                                                                                                                                     /note="synonyms: SLAP2, E
/db_xref="LocusID:77799"
/db_xref="MGI:1925049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAH52655.1"
|db_xref="G1:30851668"
|db_xref="LocusID:77799"
                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
product="Sla2 protein"
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      db xref="taxon:10090"
                                                                                                                                                                                                                                                                        gene="Sla2"
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                                                                                                                                                                                                                                                                                        Straubberg, R.L., Feingold, E.A., Grouse, D.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.R., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Schuler, G.D.,
Altschul, S.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonando, M.F., Casavant, T.L.,
Scheefz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Morarin, P.J.,
McKernan, K.J., Malek, J.A., Qunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodersgren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Retteman, M., Madan, A., Young, A.C., Sherchenko, Y.
Bouffard, G.G., Blakesley, R.W., Tuchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J. Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 112 Row: e Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;

Wab site: http://www.nisc.nih.gov/
Contact: nisc.mgc@apt.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeeley,R.W., Boutfard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Hadjighi,P., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduco,Q.L., Masiello,C., Maskeri,B., Mastrain,S., Naclobskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 1384)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Drs. Dennis Taub, Dan Longo (NIA, USA),
Jonathan Keller (NCI, USA)
CDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/)
DNA Albrary Arrayed by: The I.M.A.G.B. Consortium (LLML)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
   us musculus Src-like-adaptor 2, mRNA (cDNA clone MGC:60811
.WAGB:30040401), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Location/Qualifiers
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Mus musculus
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                                                          BC052655
BC052655.1 GI:30851667
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KEYWORDS
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ORGANISM
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TITLE
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442 573 502 562

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Arzuy467 11348 bp mRNA linear ROD 03-JUN-2002
Mus musculus Src-like adaptor protein-2 mRNA, complete cds.
AF287467
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Mus musculus
Eukaryotalus
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa, Chordata; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 1348)
In (bases 1 to 1348)
Inreto,M.P., Berry, D.M. and McGlade, C.J.
Functional cooperation between c-Cbl and Src-like adaptor protein:
In the negative regulation of T-cell receptor signaling
Mol. Cell. Biol. 22 (12), 4241-4255 (2002)
                                                                                           454
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Loreto,M.P. and McGlade,C.J.
Direct Submission
Submitted (14-JUL-2000) Brain Tumour Research Centre, Hospital
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Conservative 0; Mismatches 191;
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/organism="Mus musculus"
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/db xref="taxon:10090"
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Patent: W 0242452-A 1 30-MAY-2002,
The Hospital for Sick Children (CA)
Location/Qualifiers
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LDRSLLFLEAPASGEASLLSEGLRESLSSYISLAEDPLDDA"
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Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada Location/Qualifiers
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/organism="Mus musculus"
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552. .824
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The invention relates to an isolated polypeptide (NOVX) a mature form of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 98; 263pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200216599-A2
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12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	10.4	10.4	10.4	10.4	10.4	10.1	10.1	6.9	6.9	9.3	9.3	9.3	9.3
141.8	141.8	141.8	141.8	141.8	141.8	141.8	141.8	141.8	123	123	123	123	123	119.4	119.4	110.6	110.6	110.6	110.6	110.6	110.6
24	25	26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; cell signal processing disorder; metabolic pathway modulation disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; acquired immunodeficiency spudfrome; AlDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Shimkets RA; ; R; R, SI Yang I Grosse WM, Hart M, Kekuda Tomlinson JE, Topper JN, hypertension; congenital heart defe Albright hereditary osteodystrophy. Human cDNA encoding protein NOV13 ABK61465 standard; cDNA; 1183 BP. 25-AUG-2000; 2000US-0228191P. 08-FEB-2001; 2001US-0267300P. 20-FEB-2001; 2001US-026951P. 20-MAR-2001; 2001US-026951P. 27-AUG-2001; 2001WO-US026510. (CURA-) CURAGEN CORP. (CORT-) COR THERAPEUTICS INC. (first entry) Conley PB, Szekeres ES, WPI; 2002-280937/32. P-PSDB; AAU91308.

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conciding NOYX (or its complement, fragment or variant). NOYX is NOV1-14, 150, 16a, and 16b. The NOYX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NOYX-associated disorder in humans, e.g. cardiomyopathy, a chercal solution of the preventing or preventing (e.g. by gene thersolerosis, a disorder related to call signal processing and antibolic pathway modulation, diabetes or cancers. The NOYX polypeptide and nucleic acids are also useful for determining the presence of predisposition to the diseases. The NOYX nucleic acid and polypeptide are especially useful in therapeutic or prophylactions for disorders associated with aberzant NOYX expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus (cancers), immune response, graft-versus-host disease, hypertension, cancers, immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defects, multiple sclerosis, inflammation or Albright pereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present
       the nucleotide
(differing by no more than 15%),
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Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 U; 0 Other;

540 360 420 480 540 900 099 180 240 240 009 120 180 TCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCCA 300 300 GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC 360 credaridarecricidadrecreredereaddaacaareddaadrereecaadaad 420 480 GTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGTATAACATCCCCAGCGTCCACGTGGG 660 CCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGCTTCCCCAGTCCAGAATCCCTAAGGAG 120 9 TCCTAGGACCAAGGACACTGGGAGACTTCCAGAAGGGCCCCCAAAGCCTTAACCTGTCCA GTGGACGGTGCTGTCTGAAGTCTCAGGCAGAAGTATAACATCCCCCAGCGTCCACGTGGG AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGGCCCTGGG cerrecerederesecreteerreseasesraceaserreceasereseases ACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTG Acceaaaccaaccracererecereaagareerecaagergaagagricraggrig GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC CTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGAAGTCTGCCCAGCAGAAG AAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCAT GGAAGCAGAGAAAGCAAGGCCACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCCC GGAAGCAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCCC GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGTGAGGATGGAGACTG GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGTAGGATGGAGTTG ; 0 Length 1183; Indels Score 1183; DB 6; Pred. No. 1.6e-310;); Mismatches 0; ö 100.0%; Matches 1183; Conservative Query Match Best Local Similarity 121 541 61 61 121 181 181 241 241 301 301 361 361 421 481 481 541 601 421 601 g В ò B à d ò g δ Оþ δ g δ 셤 ò g ò ò $\stackrel{>}{\circ}$

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qq	841 CAGGALCCACTGCCTTGACAATGGCTGGCTGTTCTCTCACCGCGCCTCACCTTCCCCTC 900
ð í	ACTCCAGGCCTGGTGGACCATTACTCTGAGCTGGGGATGACATCTGCTGCCTACTCAA 96
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ò	1141 CATCAGCCTGAATGACGAGGCTGTCTTTGGATGATGATGCCTAG 1183
qq	1141 CATCAGCCTGAATGACGAGGCTGTCTTTTGGATGATGCCTAG 1183
RESUJ AAD4:	LT 2 3980
X X S	AAD43980; CDNA; 236; DF.
XX	EC-2
X E	Human Src-Like Adapter Protein-2 (hSLAP-2) cDNA.
X & & &	Human, SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2; SLAP-2; immune disorder; signal transduction; autoimmune disease; cancer; nachlasm. inflammation disorder. rheumatoid arthritis.
KW KW	psoriasis, rhinitis, allergy; inflammatory bowel disease; gene therapy; crohn's disease; systemic lupus erythematorus; tissue/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective; gene; ss.
X 8 i	Homo sapiens.
Y E E E	Key Location/Qualifiers CDS 415.1200
E >	/reag- a "Human SLAP-2"
Y II.	WO200242457-A1.
{£\$	30-MAY-2002,
(E)	20-NOV-2001; 2001WO-US043367.
PR X	22-NOV-2000; 2000US-0252545P.
₽X	(BRIM) BRISTOL-MYERS SQUIBB CO.
PI	Chang H, Yang W, Wu Y, Whitney GS, Perez-Villar JJ, Kanner SB;

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The invention relates to a substantially purified human SH2/SH3-domain-
containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-
2). The invention is useful for treating an immune disorder involving
hyperactivity of B- or T- lymphocytes in a mammal. The invention is
useful for screening for antagonists or inhibitors of the interaction of
hSLAP-2 with cellular signalling compounds, for disgnosing, treating or
nolecules which associate with hSLAP-2 and which provide critical signals
or cellular signal transduction, for determining those cellular signalling
molecules which associate with hSLAP-2 and which provide critical signals
or cell activation, and as effectors in methods to affect T cell
activation. The invention is useful in screening assays to identity and
activation. The invention is useful in screening assays to identity and
cettor candidate bloactive agents that modulate hSLAP-2 bloactivity, for
potential use to treat autoimmune diseases which may be caused
by hyperactivated B cells, in addition to other immune system related
conditions, diseases and conditions, theumatoid arthritis,
osteoarthritis, psoriasis, rhinitis, inflammatory bowel disease (Crohn's
and ulearative collish), and T-cells and B-cell moplasms,
inflammation disorders, diseases and conditions, theumatory disease such as systemic lupus
ast cells or eosinophils, autoimmune diseases such as systemic lupus
asthma, acute respiratory distress syndrome, and chronic obstructive
cuseful in gene therapy. The present sequence is human SLAP-2 CDNA
                                                                                                        ng adapter
therapeutic
                                                                                                   Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeut intervention in immunological and inflammatory disorders and cancer.
                                                                                                                                                                                                            Claim 2; Fig 1; 85pp; English
                         WPI; 2002-463632/49
                                                P-PSDB; AAE26357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human modulator of antigen receptor signalling protein coding sequence.
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GGAAGCAGAGAAGCAAGGCCACAGGCCGTGGCCCTGGGCCAGTTTCCCGGCAGGTGGCCC
                                                                                                                     GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGACTG
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The present sequence encodes the human Src-like inhibitory molecule (SLIM) protein (1). The present invention describes a SLIM protein comprising an N-terminal myristylation sequence, an N-terminal SH2 domain, and an N-terminal SH3 domain which can bind to Cbl, or comprising an N-terminal myristylation sequence and an N-terminal SH2 domain which is unable to bind to Cbl. (1) has antiinflammatory, immunosuppressive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Src-like inhibitory molecule, SLIM, Src-like adapter protein, SLAP; inhibitor; antiinflammatory; immunosuppressive; anti-HIV; andulator; Iymphocyte; (Dl) gene therapy; immunodeficiency disorder; acquired immune deficiency syndrome; AIDS; actte inflammatory disorder; chronic inflammatory disorder, autoimmune disorder; ransplant rejection;
GATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCCCT
                                                                                                                                                                                                                           CTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTGGATGAT
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                                                                                                                                              GACAGCTCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New src-like inhibitory molecule protein, useful for treating immunodeficiency disorders and inflammatory disorders, comprises terminal myristylation sequence, SH2 domain and/or SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Src-like inhibitory molecule (SLIM) encoding cDNA.
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product= "SLIM"
/note= "Src-like inhibitory molecule"
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                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor game and exhibits structural and sequence similarity to the Sor-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present CDNA sequence encodes a human MARS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGGCCAGGGACCTGTGACCATGGAAGCAGAGAAGCAAGGCAAGACAAGGCCACAGAGCGTGGCCCTG
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Pred. No. 1.9e-202;
0; Mismatches 1;
                                                                                                                                              HOSPITAL FOR SICK CHILDREN
                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 75; 110pp; English
                                                             26-NOV-2001; 2001WO-CA001662
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99.9%;
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                                                                                                                                                                                                                                                                                                                                                    Cytostatic; Cardiant; Anti-allergic; Immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 953; 78pp; English.
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                                                                                                                                                                                                  ABQ98670 standard; DNA; 763 BP
                                                                                                                                                                                                                                                                                                               Human ORF477 coding sequence.
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                                                                                                                                                                                                                                                                           (first entry)
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(MEHR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
                                                                  GCCTAG 1183
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Matches 760;
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activation, and can be used as a modulator of lymphocyte activation, and of ubiquitination of a CDI target protein, and in gene therapy. (I) is useful for screening a bioactive agent capable of binding to SIIM. (I) is also useful for screening a bioactive agent capable of colling the treatment of conditions which involves this function or dysregulation of SIIM protein activity. i.e. to diagnose, treat or dysregulation of SIIM protein activity. i.e. to diagnose, treat or prevent SIIM associated disorders. (I) or the polymuclectide encoding it conducting antigen receptor-induced signalling and activation, for modulating antigen receptor-induced signalling activity of lymphocytes. (I) or is also useful for modulating the basal activity of lymphocytes. (I) or (II) is useful in the treatment of immunodeficiency disorders, such as caquired immunodeficiency syndrome (AIDS), for the prevention and treatment of acute inflammatory disorders, chronic inflammatory. Consequence of inflammatory disorders, chronic inflammatory activation in treatment of incurrence 
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New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
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                                                                                61 GCTGAGCTACCCAAACCACCTAGCCTCTCTCTGAAGATCCTCCCAGGCTGAGAGAGT
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antiposriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimmlant; thrombolyvic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; Human ORFX ORF2757 polynucleotide sequence SEQ ID NO:5513 AAC77202 standard; cDNA; 837 (first entry) 08-FEB-2001 RESULT

242

AGTCTCAGGCAGAGAGTATAACATCCCCAGCGTCCACGTGGCCAAGTCTCCCATGGGTG

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: oytostatic, hepatotropic; vulnerary; actipacialist; antiparkinsonian; nootropic; neuroprotective; osteopathic; antipachiant; immunosuppressant; immunostimulant; cardiant; htmombolytic; cagaliant; passtropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidifamentory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors: The proteins and nucleic acids may be used to treat cancers, proliferative disorders, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune cartialage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
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02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-01277336P.

30-MAR-2000; 2000US-00540763.
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P-PSDB; AAB42993.
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                                                                                  Homo sapiens.
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le AJ, Yang Y, Wehrman T, Drmanac RT;
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N-PSDB; ABP64788.
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The present invention relates to novel human coding sequences (ABQ99268-ABQ9608) and proteins (ABP64682-ABP6502). The sequences are useful in thereared in the field of molecular biology as hybridisation probes, primers consequence, for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The proteins are useful in diagnostics as expressed sequence tags of protein, or in generation of anti-sense DNA or RNA. The production of anti-sense dense or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins way be used to maintain condexisted or supplements. The proteins may be used to maintain condexides and proteins are useful for preventing is transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The cuseful for preventing broteins are useful for preventing, treating or amelioration disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral cuseful, bacterial or fungal infection, autoimmune disorders, allergic reactions and conditions, coagaliation disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic conditions and conditions, coagaliation disorders, or cancer. The sequence of the invention were assembled from STFs isolated mainly by sequencing by hybridisation, and in some cases, cata for this patent did not form at at the printed specification, but manner disorders and in some cases. The sequence of the invention were assembled from the sequence of the invention and in some cases.
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disorders involving
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New isolated polynucleotide, useful in research, di
therapeutic methods, e.g. preventing or treating di
aberrant protein expression or biological activity.
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                                                                                                                                                                                             Claim 1; SEQ ID NO 107; 394pp; English
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myeloproliferative disorders and

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disorders, immunosuppression,
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                                                                                                                                                                                                                              AGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTTGGATGATGCCTAG 789
                                                                                                                                                                                                                                                                                                                                                                         receptor signalling;
CCTCCTGTTTTCTGAAGCTGCCACAGGGAAGATCTCTTTTTTCTAAGAGGTCTCCCGGG
                                                                            TCTGCTGCCTACTCAAGGAGCCCTGTGTCTCCTGCAGAGGGCTGGCCGGCTCCCTGGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                         Mouse; gene; ss; gene therapy; modulator of antigen receptor signalli; MARS; tumour suppressor gene; Scr-like adaptor protein; SLAP; myelodi malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    short isoform protein'
                                                     541 GCCTCACCTTCCCCTCACTCCAGGCCTGGGGGGGCCATTACTCT----
                                                                                                                                                                                                                                                                                                                                                    Mouse MARS short isoform protein coding sequence.
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malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a mouse MARS protein
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Matches 734; Conservative
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                                                                                        595 AGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGTATAACATCCCCAGCGTCCA
                                                                                                                                            1162 AGACTGGTGGACGGTGCTGTGAAGTCTCAGGCAGAGAAGTATAACATCCCCAGCGTCCA
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                DNA encoding novel human diagnostic protein #10554
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                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of modula of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of
                                                                                                                                                                                                                          New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1348 BP; 324 A; 385 C; 362 G; 277 T; 0 U; 0 Other;
HOSPITAL FOR SICK CHILDREN
                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 1A; 110pp; English.
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Best Local Similarity 78.23
Matches 714; Conservative
                                                                Loreto MP;
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P-PSDB; AAO15456.
                                                            Mcglade JC,
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the vibo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGAGCCTGTGTGTCCTGCAGAGGCTGGCCCCCTCCCTGGCAAGGATATACCCCTACCT
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                                                                                                                                     Sequence 603 BP; 124 A; 189 C; 164 G; 126 T; 0 U; 0 Other;
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23-AUG-2000; 2000US-00649167.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed environment of its useful in gene therapy techniques to restore normal crivity of (II) as useful in gene therapy techniques to restore normal extivity of (II) at to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS4454 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WND at the printed specification, but was obtained in electronic format directly from WND at the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 CCCTGGGCCTTCCCTCCCTGGCTCGGCTGTCTTGGGAGGGTTCCCCAGTCCAGAATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 CGCTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGTCCAGAATCCC
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                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                       Claim 1; SEQ ID NO 10551; 103pp; English.
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Best Local Similarity 98.6
Matches 409; Conservative
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(MEHR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
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P-PSDB; ABP64588.
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Matches 341;
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                                              Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary, Antiniflammatory, gene therapy, human; ORFX; atherogenic; platelet, human umbilical vein endothelial cell; HUVEC, atherosclerotic plaque, cancer; cardiovascular disease, allergy; autoimmune disease, wound healing; blood coagulation disorder; inflammatory disorder; ds.
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29.4%; Score 348; DB 6; Length 444;
Best Local Similarity 100.0%; Pred. No. 3.7e-84;
Matches 348; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 951; 78pp; English.
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                Human ORF476 coding sequence.
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MEHRABAN F.
CONLEY P B.
TOPPER J N.
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241 GAAGCAGAGAGAAAGCAAAAGGCCACAGAGGCCCTGGGCAGTTTCCCGGCAGGTGGCCCG
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                                                                                                                                                                                        GCCGAGCTGTCGCTGAGACTCGGGGGGCCATTGACCATCGTCTCTGAG
                                                                                                             GCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAG
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                           2 GGATCCACTGCCTTGACAATGGCTGGTACATCTCACCGCGCCTCACCTTCCCCTCAC 61
                                                                                                                                               122 AGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGA
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                                                            903 TCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAGG
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of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymototide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at five. The sequences of the invention are appear in the printed specification, but was obtained in fip.wipo.int/pub/published_pct_sequences
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Job time : 1105 secs
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Matches 193; Conservative
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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gb gssl: *
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1183
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2: em_esthum:*
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7: em_estron:*
9: gb_estl:*
10: gb_est2:*
11: gb_est2:*
11: gb_est3:*
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11: gb_est6:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ALS41041 ALS41041	BQ054281 AGENCOURT	BQ052308 AGENCOURT	BO052468 AGENCOURT
SUMMARIES	ΠD	921.4 77.9 1201 9 AL541041	BQ054281	BQ052308	BO052468
	DB	6	12	12	12
	Query Match Length DB ID	1201	1020	1002	1069
dю	Query Match	77.9	72.7	69.1	61.8
	ult No. Score	921.4	860.2	817	731.4
	Result No.	ч	~	m	4

BC1784 BC0534 BC0534 AC0308 BX3836 AC0208 BC2841 BC2841 BC2841 BC3841 BC3841 BC3841 AL84430 AL84430 BC1915 BC1915 BC1915	6.533 CB426333 601508 MA 18999 B1998999 480839 MA 1055 A1510095 mj42604.y 1005 B6677567 602624118 13006 B6015229 127457 MA 13005 B6015229 127457 MA 13005 B6015229 127457 MA 13006 B6015229 127457 MA 13006 B6015229 127457 MA 1300 B744306 B7849096 1310 A244306 B7849096 1311 A1844312 A1844312 1312 A244312 A1844312 1314 B771720 tal6a01.x 1314 B771720 tal6a01.x 1315 B741149 BX416149 1316 B071774 AL549826 1310 B071774 AGENCOURT 1310 B071774 AGENCOURT 1311 B7769183 603053793 1311 A1844310 A1844310	ALIGNMENTS 1201 bp mRNA linear EST 12-MAY-2003 PLACENTA Homo sapiens cDNA clone CSODE005YK23 ordata; Craniata; Vertebrata; Euteleostomi; imates; Catarrhini; Hominidae; Homo issee, J. and Polayes, D issee, J. and Polayes, D issee, J. and Polayes, D inal de Sequencage ax - France e.cns.fr, Web: www.genoscope.cns.fr d by Life Technologies, a division of this cluster, see ang@lifetech.com URL :
0 0 0 0 0 0 0 0 0	4 CB426333 2 BG679593 2 BG679599 3 BE0533005 3 BE0533005 3 BC533005 3 BC533005 4 AL844310 4 AL844310 9 AY41527 3 BA71720 3 BA71720 3 BA71720 3 AL844310 3 AL844310 3 AL844310 3 AL844310 3 BA71720 3 BA71720	ALIGNN 1201 k 1201 k 14829 1) Chordata; primates; Jessee,J. Libraries and Rational de Rational de Rational de Rational de Rational de Roder - Fran Gope. Cns. fi Gouerd by Lii Gout this cl 8. ens. fran Gout this cl
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	0 0 00 0	RESULT 1 AL541041 LOCUS DEFINITIC ACCESSION VERSION KEYWORDS SOURCE ORGANIS ATTHUR AUTHORS JOURNAL TITLE JOURNAL COMMENT

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ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/ANOI sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                  BQ054281 1020 bp mRNA linear EST 29-MAR-2002 AGENCOURT_6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936362 5', mRNA sequence.
BQ054281.1 GI:19813621
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                                                                                                                                   L (Dases I to Lutur)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDM Library Preparation: Rubin Laboratory

CDM Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Dh Sequencing by: Agencourt Blossience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2125 row: j column: 11

High quality sequence stop: 556.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
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     TTACTCTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGGGACCGGATCAGACACTACAG
                                                                                                        GATCCACTGCCTTGACAATGGCTGGGCTGTACATCTCACCGCGCCTCACCTTCCCCTCACT
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                                                                                                                                                                                                                                         CCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGA 942

    1020
    organism="Homo sapiens"

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AUTHORS
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                                                                                             /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE005YK23"
/tissue type="PLACENTA"
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Library was not normalized."
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE005AF12QP1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        77.9%; Score 921.4; DB 9; Length 1201; 97.9%; Pred. No. 1.5e-221; ive 12; Mismatches 8; Indels 0;
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Best Local Similarity
Matches 919; Conserv
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o
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: Gapbs-T@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2118 row: d column: 23
High quality sequence stop: 670.
Location/Qualifiers
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Mammalla, Butheria, Primatee, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1002)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                    GATGTGCTTCTGAGTGCTCTGCTGAAGAAACAATGGGAAGTCTGCCCCAGCAGAAAAATC
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599 Qy 310 TGCTCTC	1 40	659 QY 370 GIGCTICTG 1021 Db 61 GIGCTICTG	Q.Y.	1 Db 121	Qy 490	1138 Db 181 GAGAAGCAA 839 Qy 550 GTCGCTGAG	Db 241 GTCGCTGAC	Qy 610 GCTGTCTGP	• Db 301 dcfafcfd	2002 670 CCATGGGTG	22 Z2		T 067	Db 481 T	QY 850 CTGCCTTGA	DD 541 CTGCCTTG	016	109	100		Db 624	Qy 1029 AGAGGACAG	Db 672 AGAGGACAC	QY 1089 CA-GGGGA		Qy 1147 CCTGAATG		E THIS	BG178487 LOCUS	
	CTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAG	CTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAG GAGCCCTGTGTCCTGCAGAGGGCTGGCCGCTCCCTGGCAAGGATATACCCCTACCTGG	GAGCCCTGTGTCCTGCAGAGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTG	ACTOTGCAGAGACACCACTCAACTGGAAAGACTGGACAGCTCCCTCC	TGCAGAGGACACCACTCAACTGGAAAGAGCTGGACAGCTCCCTCC	GCTGCCACA-GGGGAAGAACTCTTCTCAGTGAGGGTCTCCGGGAAGTCCTCAGCTTC	TACATCAGCCTGAATGACGA-GGCTGTCTCTGGATGATGCC 1180	TACATCAGCCCTGATGACGAGGGCTGTCTTTGGATGATGCC 882		68 1069 bp mRNA linear EST 29-MAR-2002	5', mRNA sequence. BQ052468	68.1 GI:19811808	Homo sapiens (human) Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Rmail: coaphs-r@mail.nib.gov	Procurement: Dr. Baniel McVicar, DBS/NCI	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be	through the I.M.A.G.E. Consortium/LLNL at: //image.llnl.gov	LLCM2118 row: n column: 13	<pre>juality sequence stop: bs1. Location/Qualifiers</pre>	11069 /organism="Homo sapiens"	/mol_type="mRNA" /db_xref="taxon:9606"	/clone="IMAGE:5933772" /tissue_type="natural killer cells, cell line"	/lab_host="DH10B (phage-resistant)" /clone lib="NIH MGC 106"	/note="Organ: blood, Vector: pOTB7; Site_1: XhoI; Site_2: BOORI; ODDA made by Oligo-dr priming. Directionally cloned into Fromit with a first sites using the following K, adaptor:	GGCACGAG(G). Library constructed by Ling Hong in the	porkelow, neing 700-000 symthosis kit (Stratagens) ,
 Db 540 AC	902	Db 600 CT Qy 962 GA	099	1022	720	Oy 1082 GC Db 780 AC	Qy 1139 TA	Db 840 TZ	4 T.III.	68 TTOM		VERSION BOOS			REFERENCE 1 AUTHORS NIH-			T. I.	200	DN. Cl	fou	P19		source						

Gaps

Query Match
61.8%; Score 731.4; DB 12; Length 1069;
Best Local Similarity 94.0%; Pred. No. 1.4e-173;
Matches 824; Conservative 0; Mismatches 1; Indels 52;

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778 bp mRNA linear EST 06-FEB-2001
F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4429896 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCCCTCGATGAT
                 AGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCCCTCGATGAT
                                                                                                                  CAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCATGGAAGCAGA
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1 (bases 1 to 778)
                            1 (bases 1 to 778)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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Best Local Similarity 96.8'
Matches 730; Conservative
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/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: bl
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

In (bases 1 to 986)
In (base 1 to 9
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AGENCOURT_6830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936339
5', mRNA sequence.
598
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Pred. No. 3.4e-156;
0; Mismatches 4; Indels 6;
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/db_xref="taxon:9606"
/clone="IMAGE:993525"
/tissue type="natural killer cells, cell line"
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/clone="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhOI sites using the following 5: adaptor:
GGCAGGG(3). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 ACGGIGCIGICIGAAAICICACGCAGAGAGIAIAAACAICCCCAICGICCACGIGGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 GAGCAIGCGICTCAGCAGAGCTGICTICCCAAGCCTTIGAIGACAAACCAAITICCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AAACCAACACTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTGTCCT
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Location/Qualifiers
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Best Local Similarity 95.43
Matches 660; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E (Dassel 1 to 878)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausherg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procuremen: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM122 row: 1 column: 06

High quality sequence stop: 394.
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                GTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCC
                                                                                                                                          AGCCAGAGCATGCGTCTCAGCAGGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTC
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            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 AGGGCCCCCAAAGCCCTAACCTGTCCAGCAGAGCATGCGTCTCAGCAGAGCTGTCTTCC 333
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                                                                                                                                                                                                                                                                            Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.

Lough S63-573 (2002)

Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Sachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Ishi, Y., Itoh, M., Kagawa, I., Kaukawa, T., Hori, F., Imotani, K., Ishi, Y., Kondo, S., Konno, H., Kouda, M., Kolima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nashi, K., Nomura, K., Numazaki, R., Ohno, M., Obsaco, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shibata, S., Shibata, S., Shibata, S., Shibata, S., Shibata, S., Shizaki, T., Yasunishi, F., Takaku-Akahira, S., Maranaten, M., and Manishi, M., Tomaru, A., Toya, T., Yasunishi, A., Muranaten, M., Jana, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                    MUST MERCALLUS 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430023D24 product:MODULATOR OF AK088672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Matshiki,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Encyclopedia Project of Genome Exploration Research Group in Riken
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK030877 2974 bp mRNA linear HTC 18-SEP-2003 Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830437Kl0 product:MODULATOR OF ANTIGEN RECEPTOR AK030877
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                         46.2%; Score 546.8; DB 1:
99.5%; Pred. No. 4.6e-127
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Invitrogen. This sequence blongs to sequence cluster 9825.r For http://www.genoscope.cns.fr/

Cgi-bin/cluster.cgi?eeq=CSODJ013BF05QPl&cluster=9825.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODJ013BF05QPl.
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Full -length cDNA libraries and normalization

Unpublished (2001)
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                    CATCCGGGAGCCAGACCAGGAGGCTCTTACTCTGTCAGTCCGCCTCAGCCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAACTGGAAAGAGCTGGACAGCTCCCTCTTTTTCTGAAG----CTGCCACAGGGGAG 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTACTCTGAGCTAGCAGATGGCATCTGCTGTCCCCTCAGGGAGCCGTGTGTCCCTGCAG 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 AAGCTTGGGCCACTACCTGGCAAAGATACACCTCCACCTGTGACTGTGCCAACATCATCA 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 AGCTTGAGTTCCTCTGTCCAAGGCCAGGACCTGTGACCATGGAAGCAGAGAAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 GTCACAGCTGTGGGCCCTGGGCAGTTTCCCAGCTGAACAGGCCAGACTATCTCTGAGA
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                                                                                                                                                                                                                                                                                                                                                                      45.5%; Score 538.6; DB 11; Length 2974; llarity 80.9%; Pred. No. 1.5e-124; Conservative 0; Mismatches 148; Indels 6;
               100%length, match=777)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation
of 60,710 full-length cDNAs

Lofe for 770 full-length cDNAs

Lofe (Dasse) 1 to 2974)

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Radchi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Harangaki, T., Hara, A., Hashiume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Miraoka, T., Kasukawa, T.,
Katoh, H., Kawai, J., Kojimi, Y., Kondo, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, Y., Kondo, S., Kurihara, C., Sakai, K., Sakai, K., Sakazume, N.,
Sagabe, Y., Taqami, M., Taqawa, A., Takaku, T., Takaku, T.,
Muramatsu, M. and Hayshizaki, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Direct Submission
               genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-ULI-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kromo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., 195hi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahki, M., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="thymus"
'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; MODULATOR OF ANTIGEN RECEPTOR SIGNALING MARS (SPTR|AAL38196, evidence: FASTY,
         of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
prepare full-length cDNA libraries for rapid discovery Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase
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Please visit our web site for further details.
UKL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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db_xref="MGI:2394046"
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clone="5830437K10"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20530913
                                                                                         11042159
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSIÓN

REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS

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RESULT 11
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LILLIAGE DESCRIPTION OF THE PROPOSED OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OF THE OFFICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB32223.1"
/db_xref="G1:12861543"
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CCPLREPCVLQKLGPLPGKDTPPPVTVPTSSLNWKKLDRSLLFLEAPASGEASLLSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue type="retina"
| clone_lib="RIKEN full-length enriched mouse cDNA library"
| dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; MODULATOR OF ANTIGEN RECEPTOR SIGNALING MARS (SPTR|AAL38196, evidence: FASTY, 100%1D, 100%1ength, match=777)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 GGGCAGTTTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGGAGCCATTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        577 CATCGICICICIGAGGAIGGAGACIGGIGGAGGGIGCIGICIGAAGICICAGGCAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           637 TAACATCCCCAGCGTCCACGTGGGCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="FANTOM_DB:A930009E21"
/db_xref="MG11911678"
/db_xref="taxon:10090"
/cloine="A930009E21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
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                                                         HTC 20-SEP-2003
                                                                                                     library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Managawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 926)
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                      Mus musculus adult retina cDNA, RIKEN full-length enriched librar clone:A930009E21 product:MODULATOR OF ANTIGEN RECEPTOR SIGNALING MARS, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakwa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramco, K., Hiracka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Marsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, K., Sano, H., Saski, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takhashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length oDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                    linear
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                         mRNA
                                                         926 bp
                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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HTC; CAP trapper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Rodezaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, M., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K., Frazer, K.S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, P., Frazer, K.S., Dalla, E., Dragani, T.A., Gariboldi, M., Gisel, C., Godsins, S., Dalla, E., Dragani, T.A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Naglett, D.B., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Ogush, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Lee, Y., Lenadard, B., Loons, P.A., Mallata, B., Macchionni, L., McKensie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pevan, W.J., Perted, G., Pescole, G., Pecco, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandellin, A., Schneider, C., Semple, C.B., Teasdale, R.D., Tomita, M., Varando, K., Wagner, L., Wahlestedt, C., Wang, Y., Warden, Y., Takenska, Y., Wang, Y., Wasaki, K., Kawai, J., Nakawa, K., Sakaki, N., Hirozane-Kishikawa, T., Wanki, Y., Mak, Y., Makawa, T., Ragwa, T., Maki, Y., Wasaki, Y., Sasaki, D., Sabibata, K., Shiraki, Y., Wasaki, Y., Sasaki, D., Sasaki, D., Shibata, K., Shiraky, R., Mayashizaki, Y., Ragwa, J., Mayashizaki, Y., Wasaki, Y., Sasaki, D., Sasaki, D., Shibata, R., Rhinsy, R., Mayashizaki, Y., Wasaki, Y., Yasunishi, A., Yasunishi, Y., Yasunishi, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY742155 RIKEN full-length enriched, adult retina Mus musculus cDNA clone A930009E21 5', mRNA sequence.
BY742155 BY742155.1 GI:27167493
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                                                                                                                                                                      ATCTTGGGACGGGATCAGACACTACAGGATACAGCGTCTTGACATGGCTGGACAGATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543
                                         CTCACCTCGCCTCACCTTCCCCTCACGCCTTGGTGGAGCATTACTCTGAGCTAGG 423
                                                                                                                                                                                                                                                                                                                                                                                                         PGCAGAGGGCTGGCCCGCTCCC 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 AGATGGCATCTGCTGTCCCTCAGGAGCCGTGTGTCCTGCAGAAGCTTGGGCCACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 İdGCAAAGATACACCICCACCIGIGACIGIGCCAACATCATCACTAAATTGGAAAAAGCT
                                                                                                                                                                                                                                                 CTCACCGCGCCTCACCTTCCCCTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     997 TGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACAGCTCCCTCCTGTTTTCTGAAG---CTGCCACAGGGGGAGTCTCTTCTCAGTGA
                                                                                                             544 GACCGCAGCCTCCTGTTTCTGGAAGCACCTGCGAGTGGGGGAGGCATCTCTGCTCAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GGGCTCCGAGAGTCCCTCCTACATCAGCCTGGCTGAGGACCCCTTGGATGATGC
937 GGATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 TTAGCCCTGG 673
                                         244
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VERSION
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BY742155
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REFERENCE AUTHORS

TITLE

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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA incredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research from In Riken Genome Computer of Reperimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse issues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/bote="Site_1: Sal1; Site_2: BamH1; cDNA library was
prepared and sequenced in Mouse Genome Envelopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="retina"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .660
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/organism="HOmo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_caref=taxon:9606"
/clone="IMAGE:4250382"
/tissue_type="adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 91"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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AL844311 GI:22019093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1079 GAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTC 1138
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Ashoroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, B.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGCTGCCACAGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGGGGAGTCCCTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      839 TACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCGCGCCTCACCTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACAGGATCCACTGCCTTGACATGGCTGGCTGTACATCTCACGGGGCCTCACCTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       899 TCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 TCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         959 AAGGAGCCCTGTGCTGCAGAGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCT
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10418 row: c column: 07
High quality sequence start: 2
High quality sequence stop: 566.
Location/Qualifiers
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCTTACTCT
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AUTHORS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 3.9e-103;
0; Mismatches 103;
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Best Local Similarity 83.4%;
Matches 538; Conservative
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AUTHORS
TITLE
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Email: humquery@sanger.ac.uk
Sanger Centre name: sccd10818.154136A
Homo sapiens EST sequence. This sequence was generated as part of
Homo sapiens EST sequence. This sequence was generated sequence
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cbNA library
are experimentally analysed using a variety of cbNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cbNA clones derived from
pool YI lib v SPB cbNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Teams/Team69/.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LiML)
Found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 322.4; DB 9;
99.7%; Pred. No. 2.3e-70;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="pool_YT_lib_v_SPD"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.3
Best Local Similarity 99.7
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1040
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BU944126
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/tissue type="adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NHH MGC_107"
/note="Cran: Preast, Vector: pOTB7; Site_1: EcoR1;
Site_2: Xhol; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhol sites using the
Directionally cloned into EcoRI/Xhol sites using the
following 5' adaptor: GGGAGGGG(0). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
C California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACATOTOACGGGGCOTOACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            933 TGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTGTCCTGCAGAGGGCTGGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 TCCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1053 AGCTGGACAGCTCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    813 CTGCATCCTGGGACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGTGT
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88.4%; Pred. No. 7.1e-70;
iive 0; Mismatches 0; Indels
         21
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he : 7840.77 secs
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High quality sequence stop: 628.
Location/Qualifiers
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Best Local Similarity 88.4
Matches 381; Conservative
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Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 86, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 25, Appl
Sequence 25, Appl
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
                                                                                                                                                                                                                                                                                                              Sequence 1, Appl:
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Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
SUBBLICANT: SUBBLICANT: SUBBLICANT: SUBBLICANT: COCKS, Benjamin G. APPLICANT: SUBBLICANT: COCKS, Benjamin G. APPLICANT: GENERAL CONFOSTION FOR THE DETECTION OF BLOOD CELL GENERALIZE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCITE PHARMACEUTICALS, INC.
                                                                        Sequence Sequence S
 Patent No.
                                     Sequence
                                                      Sequence
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MEDIUM TYPE: Flopy disk
COMPUTER: BLAND COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPACE: WAS PERCECT 6.1 FOR WINDOWS/MS-DOS
SOFTWARRE: WATCA PERFECT 6.1 FOR WINDOWS/MS-DOS
SOFTWARRE: WATCA PERFECT 6.1 FOR WINDOWS/MS-DOS
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: BFILEW DATE:
FILING DATE: FILING DATE:
FILING DATE: FALEN J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REGISTRATION NUMBER: 37,071
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REMEMBER: 30,071
REM
                                                                                   US-00-244-583-11
US-00-392-932-6
US-09-392-931-1
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PCT-US95-10973A-86
PCT-US95-10973A-86
US-08-718-904
US-09-449-249-1
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US-09-244-583-25
US-09-037-983C-14
               US-08-306-691B-28
US-09-860-473-17
PCT-US93-06251-70
PCT-US95-10973A-18
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5219739-21
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CLONE: 9183911
US-09-023-655-1105
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US-09-023-655-1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Sequence 1105, Ap
Sequence 1158, Ap
Sequence 1080, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1452, Ap
Sequence 3, Appli
Sequence 3, Appli
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Sequence 77, Appl
Sequence 77, Appl
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                                                                                                                     Pebruary 19, 2004, 21:32:00 ; Search time 191.966 Seconds
   (without alignments)
   3419.919 Million cell updates/sec
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Sequence 931
Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgm2_6/ptodata/2/ina/5A_COMB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-023-655-1108
US-09-023-655-1158
US-09-016-434-1452
US-08-707-793A-3
US-08-707-793A-3
US-09-220-132-77
PCT-US93-655-1313
US-09-220-132-77
US-07-820-011A-3
US-09-860-473-3
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US-09-023-655-931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-06251-13
PCT-US93-06251-14
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US-07-820-011A-1
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US-09-470-881-2
                                                                                                                                                                                                                                                                                                                            682709 segs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                 IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                                                                             US-09-939-853A-74
1183
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Match Length
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Maximum DB seq
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119.4
110.4
107.4
101
92.6
91.6
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Perfect score:
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                                                                                   OM nucleic
                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                       Run on:
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634 GTATAACATCCCCAGGGTCCACGTGGGCAAAGTCTCCC---
                                                                                                                                                                                                                                                                                                           Score 119.4; DB 4;
Pred. No. 1.8e-24;
0; Mismatches 236;
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Strart.
APPLICANT: Jeffrey J. Seilhamer
IIILE OF INVENTION: COMPOSITION FOR THE DETITION OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: S174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                               PA-0001
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Patent No. 6607879
                         REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1158:
SEQUENCE CHARACTERISTICS:
LENGTH: 2298 base pairs
             37,071
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.3
Matches 283; Conservative
                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                   ; CLONE: 9187268
US-09-023-655-1158
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                                                                                                                                   517 GGGCAGTTTCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGAC
                                                                                                                                                                                                           577 CATCGTCTCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGTA
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                                                                                                                                                                                                                                                                                   637 TAACAICCCCAGGGTCGGGCAAAGICTCCCAT------GGGTGGCTGTA
                                                                                                                                                                                                                                                                                                                       685 TGAGGGCCTGAGCAGGAGAAAGCAGAACTGCTGTTGTTACCTGGGAACCCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                              543 CAAGGGCATCAGCCGGAAGGACGCAGAGCGCCAACTGCTGGCTCCCGGCAACATGCTGGG
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                                                           CCAAGGCCAGGGACCTGTGACCATGGAAGCAGAGAAGCAAGGCCACAGCCGTGGCCCT
                                                                                               303 CAACAGCAACACACCAGGAATCAGGGAGGCAGGCTCTGAGGACATCATCGTGGTTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE DETECTION OF BLOOD CELL GENE
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     Pred. No. 1.5e-25;
0; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR 'ITTLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ? Sequence 1158, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for W
     53.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                           Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CALIFORNIA
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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682 GTATGAGGGCCTGAGCAGGGAAAGCAGAGAACTGCTGTTGTTACCTGGGAACCCTGG 741
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                                                                                           Gaps
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                                                                                      12;
Length 2298;
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506 573 626

633

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570 CATTGACCATCGTCTCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 TGGCCCTGGGCAGTTTCCCGGCAGGTGGCCCGAGCTGTCGCTGAGACTCGGGGAGC
       COMPOSITION FOR THE DETECTION OF SIGNALING PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 2129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107.4; DB 4; Length Pred. No. 4.9e-21; 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPALIANCE COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2
TITLE OF INVENTION: COMPOSITION FOR THE TITLE OF INVENTION: PATHWAY GENE EXPRES NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, IN STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Fellec, C. CURRENT APPLICATION NUMBER: US/09/016,434
PILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION NUMBER:
TLASSIFICATION NUMBER: 37,071
RECISTRATION NUMBER: 37,071
RECISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 U.
TELEPHONE: (650) 845-466
INFORMATION FOR SEQ ID NO: 1452:
SEQUENCE CHARACTERISTICS:
LENGTH: 2129 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    COUNTAL
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
FounTTER: IBM PC compatible
PC-DOS/MS-T
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53.2%;
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Best Local Similarity 53.2
Matches 259; Conservative
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US-09-016-434-1452
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LIBRARY: GENBA
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Pred. No. 9.2e-22;
0; Mismatches 170; Indels 1
                                             COMPUTER TEXABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPOPPY disk
COMPUTER: PROPER FOLDS MS-DOS
SOFTWARE: WORD PErfect 6:1 for Windows/MS-DOS 6:2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
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CLASSIFICATION:
ATTGATEY/AGET INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERBINCE/DOCKET NUMBER: PA-0001
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-0555
ITELEPAX: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1080:
SEQUENCE CHARACTERISTICS:
LENGTH: 2354 base pairs
ITYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CLONE: 9182573
US-09-023-655-1080
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Best Local Similarity
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Gaps

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433 ACTCACGGCTCCTTCCTCATCCGGGAGAGCGGAGACCGCGGGATCGTTTTCACTGTCG 492
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                                                                                                                                                         613 ceccarradacerados de contrados de contra
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                                                               917 GACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTG
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59.0%; Pred. No. 2e-19;
tive 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08707792A
Patent No. 5783398
GENERAL INFORMATION:
APPLICANT: MARCY, ALICE
APPLICANT: SALOWE, SCOTT P.
APPLICANT: WISNIEWSKI, DOUGLAS
ITLE OF INVENTION: A HIGH THROGHPUT ASSAY USING
ITLE OF INVENTION: PUSION PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: MARCK & CO., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTER READABLE FORM:
MEDIUM TYPE: Disketer
COMPUTER: Disketer
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASISED for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,792A
FILING DATE: 04-SEP-1996
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TELEFHONE: 908-594-3902
TELEFAX: 908-594-4720
TELEX:
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ATTORNEY/AGENT INFORMATION:
NAME: Camara, Valerie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Camara, Valerie J
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 59.0
Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: N
COUNTRY:
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                                                                               679 GCATTACACCAATGCTTCAGATGGGCTGTGCACACGGTTGAGGCCGCCCTGCCAGACCC 738
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918 ACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGC 977
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Pred. No. 2e-19;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SALOWE, SCOTT P.
TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
TITLE OF INVENTION: PUSION PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0900
ZONDYTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compariable
OFBRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,793A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08707793A Patent No. 5776696 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Camara, Valerie J
REGISTRATION NUMBER: 35,090
REFERENCE/DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.0%;
Matches 173; Conservative
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MOLECULE TYPE: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908-594-4720
                                                                                                                                                                                        978 AGAGGGC 984
                                                                                                                                                                                                                                                                                        739 AGAAGCC 745
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432

Gaps

CTGTCA 796

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APPLICANT: Shyian, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
RIOR APPLICATION NUMBER: US/09/303
PRIOR PILING DATE: 1998-03-25
FILE APPLICATION NUMBER: US/0079,303
PRIOR FILING DATE: 1998-03-25
FILE APPLICATION NUMBER: US/0068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
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GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Steveospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                       1050 İTGİACAACAİTACİCAGAGAGAĞCIĞCAĞGICİÇİĞCİĞCĞGCÇIAGIAGIIÇÇÇĞT 1108
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                                          TGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTGT 970
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Pred. No. 2.9e-16;
0; Mismatches 130; Indels
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FastSEQ for Windows Version 4.0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          Sequence 77, Application US/09220132
Patent No. 6506607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.5%;
Matches 169; Conservative (
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) ORGANISM: Homo sapiens
US-09-220-132-77
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STATE: NY
COUNTRY:
                                                                                                                                                                                               09-220-132-77
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                                                                                                                                                                           Sequence 1313, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION

APPLICANT: Cocks, Benjamin G.

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: EXPRESSION

VORBES PONDENCE: 1508

CORRESPONDENCE: 1508

CORRESPONDENCE: ADDRESSE: NOCYTE PHARMACEUTICALS, INC.

STREET: 3174 FORTER DRIVE

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 AACTTGACAATGGTGGATACTACATTACCACCCGGGCCCAGTTTGAAACACTTCAGCAGC 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               930 TTTCTATCCGTGATTGGGATGATATGAAAGGAGACCATGTCAAACATTATAAAATTCGCA 989
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917 GACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTG 969
                                               613 CGCCATTACACCAAGCTTCAGATGGGCTGTGCACACGGTTGAGCCGCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 92.6; DB 4; Length 2435; ilarity 56.9%; Pred. No. 9.6e-17; Conservative 0; Mismatches 129; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672 ATGGGTGGCTGTATGAGGGCCTGAGGAGGAAAGGAAGAAGGAAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATFLACATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1313:
SEQUENCE CHARACTERISTICS:
LENGTH: 2435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inear.
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Best Local Similarity
Matches 170; Conserv
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LIBRARY: GENBANI:
CLONE: 9338227
US-09-023-655-1313
                                                                                                                                                     JS-09-023-655-1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079 GARACCCARGAGGTACCTTTTTTTTCGCGAGAGTGAAACCACCAAAGGTGCCTATTCAC 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAACCCTGGAGGGCCTTCCTCATCCGGAGAGCCAGACCAGGAGAGGCTCTTACTCTC
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APPLICANT: Madri, Joseph A.
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Untringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Biddenblial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES:
ADDRESSEE: Maurice M. Klee
SOFTWARE: Patentin Release #1.0, Version #1.25 URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 91; DB 5; Le:
llarity 56.5%; Pred. No. 2.9é-16;
Conservative 0; Mismatches 130;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
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                                                                                         APPLICATION NUMBER: PCT/US93/06251
FILLING DATE: 19930630
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Diddilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCEY/DOCKET NUMBER: 8586
TELECOMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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CITY: Fairifield
STATE: Connecticut
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COUNTRY: USA
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Best Local Similarity
Matches 169; Conserv
                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
PCT-US93-06251-77
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556 GAGACTCGGGGGAGCCATTGACCATCGTCTGAGGATGGAGACTGGTGGACGGTGCTGTC 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 90.8; DB 1; 3.4%; Pred. No. 2.6e-16; ve 0; Mismatches 182;
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Acid Sequence of the Region Coding
the Carboxy-Terminal Two-Thirds of
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US/07/820,011A
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosome 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S: Anderson, Stephen K.
S: Gibbs, Carol P.
S: Tanaka, Akio
S: Kung, Heing-Jien
S: Pulita, Donald J.
Human Cellular src Gene:
            FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLee, MAULICE M.
REGISTRATION NUMBER: 30,399
REFRENCE/DOCKET NUMBER: LB-1C
TELECOMMUNICATION INFORMATION:
TELEPAX: (203) 255 1400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibbs, Carol P.
Arthur, Richard R.
Anderson, Stephen K.
Kung, Hsing-Jien
Fujita, Donald J.
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.4%;
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Best Local Similarity 53.4°
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOSOME/SEGMENT: C:
PUBLICATION INFORMATION:
AUTHORS: Anderson, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anaka, Akio
                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: GRAMISM: HOMO SE POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogenes
                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
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AUTHORS:
AUTHORS:
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VOLUME: I
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AUTHORS:
AUTHORS:
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AUTHORS:
AUTHORS:
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Kung, Hsing-Jien
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/L
FILING DATE: 199330105
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                                                                                                                                                                                                                                                                                                                                                                                      STAIL.
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Lines-
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PUBLICATION: NFORMATION: AUTHORS: CALARA
AUTHORS: CALARA
AUTHORS: CALARA
AUTHORS: CALARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                   Connecticut: USA
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HYPOTHETICAL: NA
ANTI-SENSE: NO
438 CCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGAGTCAGAGCGGTTACTGCT 497
                                                  724 GITACCTGGGAACCCTGGAGGGCCTTCCTCATCCGGGAGGCCAGACCAGACCAGAGGCTC 783
                                                                                                 498 CAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGCGAGAAGGTGAGACCACGAAAGGTGC 557
                                                                                                                                                 784 TTACTCTCTGTCAGTCGGCCTCAGCCGCCCTGCATCCTGGGACCGGATCAGACACTACAG 843
                                                                                                                                                                                             558 chachechercheadarengaenregaeadeecheaageaecheaageacheheaa 617
                                                                                                                                                                                                                                               844 GATCCACTGCCTTGACAATGGCTGGTGTACATCTCACGGGCCTCACCTTGCCCTCACT 903
                                                                                                                                                                                                                                                                                            618 GATCCGCAAGCTGGACAGCGGCGTTCTACATCACCTCCCGCACCCAGTTCAACAGCCT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 GAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGACTGGTGGACGGTGTC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 GCTCAGCACAGGCAGGCTACATCCCCAGCAACTACGTGGCGCCCTCCGACTCAT 437
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Pred. No. 2.6e-16;
0; Mismatches 182; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
FILE REFERENCE: RTS-022
CURRENT APPLICATION NUMBER: US/09/660,473
CURRENT PILLING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 169
LENGTH: 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 TGAAGTCTCAGGCAGAGAATATAACATCCCCAGCGTCCACGTGG----
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Patent No. 6656732
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val Similarity 53.4%;
222; Conservative 6
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ORGANISM: Homo sapiens
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) LOCATION: (1)...(1611)
US-09-860-473-3
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Best Local S
Matches 222
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APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Warren, Stephen L.
APPLICANT: Warren, Stephen L.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burn Street
CITY: Fairfield
STATE: Connear
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the Carboxy-Terminal Two-Thirds of
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Human Cellular src Gene:
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PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen K.
AUTHORS: Glabs, Carol P.
AUTHORS: Tanaka, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/820,0
FILING DATE: 06-JAN-1992
ATTORNEY/ACBNT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: ALM
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,399
                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS 5.0 SOFTWARE: Displaywrite 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (203) 255 1400
TELEFAX: (203) 255 1400
INFORMATION FOR SEQ ID NO. 3: SEQUENCE CHARACTERISTICS:
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AUTHORS:
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732 GGAACCCTGGAGGGCCTTCCTCATCCGGGAGGCCAGACCAGGAGGGGCTCTTACTCTC
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MEDIUM TYPE: 125 inch, 360 Kb storage COMPUTER: 1BM PC XT OPERATING SYSTEM: PC-DOS/MS-DOS 2.10 SOFTWARE: Displaywite 3 SOFTWARE: Displaywite 3 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O7/820,011A FILING DATE: 19920106 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,399 REGISTRATION NUMBER: 30,399 REGISTRATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION INFORMATION: TELECHMUNICATION SEQUENCE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERISTICS: LEGISTRE CHARACTERIS
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STREET: 1951 Burr Street
CITY: Fairifield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA to MRNA HYPOTHETICAL: NO ANTI-SENSE: NO OPTITES
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M.
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STRANDEDNESS: Double
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Pred. No. 2.6e-16;
0; Mismatches 182; Indels 12; Gaps
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; Patent No. 6656732
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
; CURRENT APPLICATION NUMBER: US/09/860,473
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 10
; LENGTH: 1626
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DNA Sequence Encoding the Amino-Terminal Region of the Human c-src Protein: Implications of Sequence Divergence among src-Type Kinase
                                                                                                                                              Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.4%;
Matches 222; Conservative 0
                                                                                                                                                                                             ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
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; NAME/KEY: CDS
; LOCATION: (1)...(1626)
US-09-860-473-10
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                                                                                                                  Oncogenes
TITLE: DE
TITLE: A:
TITLE: DE
TITLE: OF
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-860-473-10
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                                         521 AGAACCCGAGAGGGACCTTCCTCGTGAGGGAGAGTGAGACCACAAAAGGTGCCTACTGCC
                                                                                                                 792 IGICAGICCGCCTCAGCCGCCCTGCAICCTGGGACCGGAICAGACACTACAGGAICCACT
                                                                                                                                                                                581 TCTCTGTATCCGACTTCGACAATGCCAAGGCCTAAATGTGAAACACTACAAGATCCGCA
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GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Marren, Stephen L.
APPLICANT: Marren, Stephen L.
APPLICANT: Luchringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endochelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: Migration
TITLE OF INVENTION: And Plasminogen Activator Activity
                                                                                                                                                                                                                                                                                                                                                                             TGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCA
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ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
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Pred. No. 2.6e-13;
0; Mismatches 136; Indels 0
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GENERAL INPORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Marren, Stephen L.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
NAME: ALSO, MAUNICATION:
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
TELECOMMUNICATION INDORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
                                                                                                                             Query Match 6.8%;
Best Local Similarity 54.4%;
Matches 162; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
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NUCLEIC ACID
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: USA
                                                                ; DATE: March, 1983
US-07-820-011A-1
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
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STRANDEDNESS:
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732 GGAACCCTGGAGGGCCTTCCTCATCCGGGAGAGCCAGACCAGGAGAGGCTCTTACTCTC 791
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Pred. No. 2.6e-13;
0; Mismatches 136;
                                                                                                                                                             AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Callular Gene Homologous to th
TITLE: Gene and the Mechanism for Gen
TITLE: Transforming Virus
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                       CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.4%;
Matches 162; Conservative
                                                                                                                 ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
                                                                                                                                                                                                                                                                                                                                                              881-890
March, 1983
Linear
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                  MOLECULE TYPE: CHYPOTHETICAL: NCANTI-SENSE: NOORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         TITLE: T:
JOURNAL:
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February 19, 2004, 23:23:34; Search time 2843.55 Seconds (without alignments) 1456.787 Million cell updates/sec
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1183
1 agctagagctccaaggaccc......tctctttggatgatgcctag 1183
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6/ptodata/2/pubpna/US07 NEW PUB.seq: *
6/ptodata/2/pubpna/PCTUS PUBCOMB.seq: *
6/ptodata/2/pubpna/US08_NEW PUB.seq: *
6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2308684 segs, 1750822206 residues
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| /cgn2_6/ptodata/2/pubpna/US07
| /cgn2_6/ptodata/2/pubpna/PCT_
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1. Appli	Sequence 21302. A	Seguence 953. App	Sequence 951. App	Sequence 1915. An	Sequence 17314. A	Segmence 499. App	Sequence 91, Appl		Segmence 15513. A	Seguence 4631. Ap	Sequence 10930. A	Sequence 2038, Ap	Sequence 1, Appli	Sequence 1983, Ap
SUMMAKIES	σI	US-10-043-649-1	US-09-814-353-21302	US-09-867-550-953	US-09-867-550-951	US-09-867-550-1915	US-09-814-353-17314	US-09-954-456-499	US-10-002-600-91	US-09-864-761-2829	US-09-864-761-15513	US-09-814-353-4631	US-09-814-353-10930	US-10-062-674-2038	US-10-193-720-1	US-09-954-456-1983
	DB	14	10	σ	σ	σ	10	Φ	13	6	6	10	10	15	15	σ
	Query Match Length DB ID	786	864	763	444	875	320	2665	3756	432	448	152	152	2343	1924	2015
ď	Query	66.3	65.5	64.1	29.4	28.8	18.0	13.3	13.3	12.0	12.0	11.1	11.1	10.5	10.4	10.4
	Score	784.4	775.4	758.2	348	341	213.4	157.4	157.4	141.8	141.8	131.6	131.6	124.6	123	123
	Result No.	н	2	m	4	ហ	9	7	80	σ	10	11	12	13	14	15

Sequence 3. Appli	7	Sequence 50. Appl	Sequence 343. App	Seguence 27, Appl	Sequence 18, Appl	Sequence 300, App	Sequence 123, App	Sequence 17, Appl	Sequence 114, App	Sequence 1776, Ap	Sequence 954, App	Sequence 1452, Ap	Sequence 1611, Ap	Sequence 15, Appl	Sequence 14, Appl	Sequence 19612. A	Sequence 25044. A	Sequence 30, Appl	Sequence 31, Appl	Sequence 512, App	Sequence 4, Appli	Sequence 19745, A	Sequence 1087, Ap	Sequence 1242, Ap	7419.	419	7419	7419	Sequence 184, App
4 US-10-007-010-3		US-10-175-523-5			5 US-10-085-117-18	US-09-967-768A-300	5 US-10-353-690-123	5 US-10-085-117-17	4 US-10-240-965-114	5 US-10-062-674-1776	0 US-09-960-706-954	US-10-305-720-1	US-09-917-800A-1611	US-10-085-117-1	US-10-085-117-	US-09-864-761-19612	0 US-09-918-995-25044	US-09-771-161A-30	US-09-771-161A-31	4 US-10-101-510-512	US-09-771-161A-4	10 US-09-918-995-19745	5 US-10-094-749-1087	15 US-10-062-674-1242	US-09-796-692-7419	4 US-10-040-862-7419	5 US-10-057-475B-7419	5 US-10-154-884B-7419	5 US-10-159-563-184
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16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	44.

ALIGNMENTS

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APPLICANT: Zhou, Xiulan
APPLICANT: Shen, Mary
APPLICANT: Shen, Mary
APPLICANT: Shen, Mary
APPLICANT: Shen, Mary
TITLE OF INVENTION: Cloning of a No. US20030059924Alel Inhibitor of Antigen-receptor & TITLE OF INVENTION: Retroviral-based Functional Screen
FILE REPERENCE: A-70019-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/10/043,649
PRIOR PILING DATE: 2002-01-10
PRIOR FILING DATE: 2001-01-10
Sequence 1, Application US/10043649
Publication No. US20030059924A1
                                                                                                                                                                                  Luo, Ying
Payan, Donald G.
Mancebo, Helena S.Y.
Wu, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 786
                                                                 APPLICANT: Holland, Sacha J.
APPLICANT: Mendenhall, Marcy
APPLICANT: Pardo, Jorge
                                                                                                                                     Spencer, Collin
Fu, C. Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS

LOCATION: (1)..(786

CTHER INFORMATION:

US-10-043-649-1
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66.3%; Score 784.4; DB 14; Length 786;

Query Match

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TYPE: DNA
ORGANISM: Homo sapiens
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                                       ATGGGAAGTCTGCCCAGCAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTC
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APPLICANT: Libompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0066B
CURRENT APPLICATION NUMBER: US/09/814,353
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                Indels
   Pred. No. 1.5e-229,
0; Mismatches 1;
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
Best Local Similarity 99.9%;
Matches 785; Conservative
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US-09-814-353-21302
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65.5%; Score 775.4; DB 10; Length 864;
Best Local Similarity 99.2%; Pred. No. 8.7e-227;
Matches 779; Conservative 0; Mismatches 6; Indels 0;
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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| NAME/KEY: misc_feature
| LOCATION: 1, 2, 3, 32, 862, 863, 8
| OTHER INFORMATION: n = A,T,C or G
| US-09-814-353-21302
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113 121 173 181 233 241 293 301

61

361 413 421 473 533 541 593 601 653 661

481

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Sequence 951, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Debbie
APPLICANT: Conley, Pamela
APPLICANT: TOpper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: WINDER: US20020082206A1e1 Polymucleotides from Atherogenic Cells and I
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
FILE REFERENCE: 21402-013 (Cura-313)
FILE REFERENCE: 2001-09-20
FRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                  GGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATCCCCCAGCGTC 540
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                               593 GGAGACTGGTGGACGGTGCTGTGTGAAGTCTCAGGCAGAGAGTATAAÇATCCCCAGCGTC 652
                                                                                                                                              CACGIGGGCAAAGICICCCAIGGGIGGCIGIAIGAGGGCCIIGAGCAGGGAGAAAGCAGAG 712
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CRGANISM: Homo sapiens
US-09-867-550-951
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US-09-867-550-951
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APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Law, Debbie
APPLICANT: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE OF INVENTION: Thereby
FILE REPERRENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR PLING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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                                     714 AAGICICCCAIGGGIGGCIGIAIGAGGGCCIGAGCAGGGAGAAAGCAGAGAACIGCIG 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGAGGAACAATGGGAAGTCTGCC 300
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                                                                                                                 722 TTGTTACCTGGGAACCCTGGAGGGCCTTCCTCATCCGGGAGAGCCAGACCAGGAGAGGC 781
                                                                                                                                                          774 ITGITACTGGGAACCCTGGAGGGCCTTCCTCATCCGGAGAGGCCAGACCAGGAAGAGG 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 CCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAAC 352
662 AAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGAGAAAGCAGAAGCAGAACTGCTG 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.1%; Score 758.2; DB 9; Length 763; 99.6%; Pred. No. 1.5e-221; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 953, Application US/09867550; Patent No. US20020082206A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      760; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                782 TCTTA 786
                                                                                                                                                                                                                                                                                        834 TCCTA 838
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US-09-867-550-953
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LENGTH: 763
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Matches
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Sequence 499, Application US/09954456

Fatent No. US2020115057A1

GENERAL INFORMATION:

APPLICANT Young, Paul

ITILE OF INVENTION: Brocess for Identifying Anti-Cancer Therapeutic Agents Using Cancord TITLE OF INVENTION: Bets

FILE REFERENCE: 689290-76

FILE REFERENCE: 689290-76

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

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PRIOR PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 GGCCCGGCCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTTCTGAGGATGGA
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Pred. No. 5.5e-
0; Mismatches
       CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/201,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PRILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 17314
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95.2%;
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Best Local Similarity 95.2
Matches 220; Conservative
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; ORGANISM: Homo E
US-09-814-353-17314
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Lopper, James
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICATION NUMBER: USSN 60/208,427
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1915
LENGTH: 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AGCCCTGTGTCCTGCAGAGGCTGGCCGCTCCCTGGCAAGGATATACCCCTACCTGTGA
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Publication No. US20030165831A1
Publication No. US20030165831A1
APPLICANT: Lee, John
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, Jamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-0068
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0
301 GCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAG 348
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28.8%; Score 341; DB 9; I
Best Local Similarity 100.0%; Pred. No. 6.5e-94;
Matches 341; Conservative 0; Mismatches 0;
                                                                                                                                                                   ce 1915, Application US/09867550 No. US20020082206A1
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                                                                                                  RESULT 5
US-09-867-550-1915
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NUMBER OF SEQ ID NOS: 116
SOFTWARE: PERL Program
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13.3%; Score 157.4; DB 9;
Best Local Similarity 54.2%; Pred. No. 1.2e-37;
Matches 354; Conservative 0; Mismatches 281;
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 499
LENGTH: 2665
                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-499
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Sequence 2829, Application US/09864761
Sequence 2829, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Pank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: According 2.1
                                                         US-09-864-761-2829
Sequence 31, Application US/10002600
Publication No. US2002013707A1
APPLICANT: Hopkins, Christopher M.
APPLICANT: Peterson, David P.
APPLICANT: Peterson, David P.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: GERES REGULATED IN ACTIVATED T CELLS
FILE REPERENCE: PA-0042 US
CURRENT APPLICATION NUMBER: US/10/002,600
CURRENT APPLICATION NUMBER: 60/243,521
PRIOR FILING DATE: 2000-10-25
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US-10-002-600-91

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                                                                                                                                                                                                                DB 13; Length 3756;
                                                                                                                                                                                                           Score 157.4; DB 13; Length
Pred. No. 1.4e-37;
0; Mismatches 281; Indels
                                                                                                                                          Template ID: 059263.15
                                                                                                                                                                                                         13.3%;
ilarity 54.2%;
Conservative
SEQ ID NO 91
LENGTH: 3756
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                    FEATURE:
NAME/KEY: misc feature
CTHER INFORMATION: Tem
                                                                                                                                                                                                                               Best Local Similarity
Matches 354; Conserv
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COTHER INFORMATION: MAP TO AL031662.24
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
US-09-864-761-15513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.0%; Score 141.8; DB 9; 95.4%; Pred. No. 4.7e-33; live 0; Mismatches 7;
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Best Local Similarity 95.4
Matches 146; Conservative
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ORGANISM: Homo sapiens
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
N: EXPRESSED IN BT474, SIGNAL = 2.4
N: EXPRESSED IN HELA, SIGNAL = 1.9
N: EXPRESSED IN HELA, SIGNAL = 2.1
N: EXPRESSED IN HELALO, SIGNAL = 2.0
N: EXPRESSED IN FEAT, SIGNAL = 1.9
N: EXPRESSED IN FEAT, SIGNAL = 2.3
N: EXPRESSED IN FEAT, SIGNAL = 2.3
N: EXPRESSED IN BAN, SIGNAL = 2.3
N: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILLING DATE: 2000-02-04
PRIOR PILLING DATE: 2000-02-06
PRIOR PILLING DATE: 2000-02-06
PRIOR PILLING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-09-07
PRIOR PILLING DATE: 2000-09-07
PRIOR PILLING DATE: 2001-01-07
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .032 GGACACTCAACTGGAAAGAGCTGGACAGCT 1064
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Best Local Similarity 95.4
Matches 146; Conservative
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RGANISM: Homo sapiens
FRATURE:
OTHER INFORMATION: EXPRE
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596 GACTGGTGGACGGTGCTGTGAAGTCTCAGGGAGAGAGTATAACATCCCCAGCGTCCAG
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TILLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFERENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US 09/62,674
PRIOR PILING DATE: 2002-01-30
PRIOR PILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL PROGRAM
SEQ ID NO 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Best Local Similarity 95.0%; Pred. No. 4.8e-30;
Matches 134; Conservative 0; Mismatches 7; Indels 0;
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10.5%; Score 124.6; DB 15; Length
Best Local Similarity 54.1%; Pred. No. 1.3e-27;
Matches 284; Conservative 0; Mismatches 229; Indels
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 411296.5
US-10-062-674-203B
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                                                                                                         PRIOR APPLICATION NUMBER: 02/09/814,353

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-05

PRIOR PILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 22037

SEQ ID NO 10930

LENGTHARE: FREESER FOR WINDOWS VERSION 4.0

LENGTHAL: 152
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Publication No. US20040005559A1
GENERAL INFORMATION:
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329 ICCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGA 388
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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: INDEMTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE REFERENCE: MRI-006B
CURRENT PAPLICATION NUMBER: US 60/191,031
PRIOR PILIOR DATE: 2000-03-21
PRIOR PELICATION NUMBER: US 60/201,124
PRIOR PILING DATE: 2000-05-25
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-05-25
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Line, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.1%; Score 131.6; DB 10; Length Best Local Similarity 95.0%; Pred. No. 4.8e-30; Matches 134; Conservative 0; Mismatches 7; Indels
                                                                                                              1032 GGACACCACTCAACTGGAAAGAGCTGGACAGCT 1064
                                                                                                                                                                                                             389 GGACACCACTCAACTGGAAGGACTGGACAGGT
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LOCATION: 17, 102, 112
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 1983, Application US/09954456

Patent No. US20020115057A1

GENERAL INFORMATION:

APPLICANT: Young, Paul

TITLE OF INVENTION: Beats

TITLE OF INVENTION: Sets

FILE REFERENCE: 699290-76

CURRENT FAPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR PLING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PLING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

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Best Local Similarity 53.9%;
Matches 283; Conservative
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APPLICANT: Wong, Brian R.
APPLICANT: Wong, Brian R.
APPLICANT: Basuda. Estaban
APPLICANT: Bowell, Mark
TITLE OF INVENTION: Modulators of Leukocyte Activation, HCk Compositions and Methods
FILE REFERENCE: A-71313/RMS/DHR
CURRENT PELLICATION UNDER: US/10/193,720
CURRENT FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
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609 CAACAGCAACACCAGGAATCAGGGAGGCAGGCTCTGAGGACATCATCGTGGTTGCCCT 668
                                              517 GGGCAGTITICCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGAC 576
                                                                                                                                            577 CATCGTCTGAGGAIGGAGACTGGTGGACGGTGGTGTCTGAAGTCTCAGGCAGAGTA 636
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                                                                                             669 GTATGATTA CGA GGCCATTCA CCAA GAA GACCTCA GCTTCCAGAA GGGGACCAGATGGT
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Publication No. US20040009173Al
GENERAL INFORMATION:
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Best Local Similarity 53.9
Matches 283; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (78)..(15
OTHER INFORMATION:
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Search completed: February 20, 2004, 05:59:08 Job time : 2861.55 secs

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February 20, 2004, 01:45:20 ; Search time 4572 Seconds (without alignments) 11214.963 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIE	CCLCANA	AX443135	AX452880	BC042041	AX511153	AX572845	AF290985	AK025645	AX780857	AX511155	AF290986	#546008	HSDJ977B1	AC026539	AX511151 AF434990	AX511150	AF287467	BC052655	AX452884	AC125701	AX443200	AX511164	AX511165	AX511166 AX511163	AC014511	AB011527	AC022349	AC018489 AC128065	AC133702	AE003503	AX443201	HSPEROTUS F24027	E24028	HUMPPRO	BC012097	AC135349 AC135349	ALIGNMENTS			1183 bp ent W00216599	555		0	Primates; Cata	Gre
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                     ACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTCAA
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Proteins and nucleid acids encoding same
Patent: WO 0216599-A 76 28-FEB-2002;
Curagen Corporation (US) ; COR THERAPEUTICS, INC. (US)
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/mol_type="unassigned DNA"
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Sequence 1 from Patent W00242457.
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                                                                                                                                                                                                                                                                                                                                               AX452880.1 GI:21712520
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
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Chang, H., Ya
Kanner, S.B.
                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AX452880
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ö TCCCCAGTCCAGAATCCCTAAGGAG 120 78 cerrecerederedesererederregadeserrececagrecadareceradadas 197 257 300 360 377 420 480 540 9 437 438 AAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCAT 497 009 77 617 GIGGACGGIGCIGICIGAAGICICAGGCAGAGIATAACAICCCCAGCGICCACGIGGG 660 720 CAAAGTCTCCCATGGGTGGTTGTATGAGGGCCTGAGCAGGAGAAAGCAGAGGAACTGCT 737 780 840 797 18 AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAAGGGCCCTGGG ACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTG 198 ACCCAAACCAACACCTAGCCTCCCCGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTG TCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAAACCTGTCCA GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC CTCGATGATGTGCTTCTGAGTGCTCTGAGGAACAATGGGAAGTCTGCCCAGCAGAAG AAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAAGGAACCTGTGAACCAT 1 AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAAGGGCCCTGGG TCCTAGGACCAAGGACTTGCAGAAGGGCCCCCAAAGCCCTTAACCTGTCCA GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC GGAAGCAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCC GTTGTTACCTGGGAACCCTGGAGGGCCTTCCTCATCGGGAGAGACCAGACCAGGGGG Gaps GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGACTG 558 GGCCGAGCTCGCTGACACTCGGGGAGCCATTGACCATCGTCTCTCTGAGGATGGAGACTG CAAAGICTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAGAAAGCAGAAGTACTGCT GITGITACCTGGGAACCCTGGAGGGCCTTCCTCATCCGGGAGAGGCCAGACCAGGAGAG CTCTTACTCTGTGAGTCGGCTCAGCCGCCTGCATCCTGGGACCGGATCAGACTTA . 0 Length 2567; Indels ., 1 9 DB Similarity 99.9%; Score 1132; D Similarity 99.9%; Pred. No. 0; 12; Conservative 0; Mismatches Query Match Best Local Simil Matches 1182; (source JOURNAL FEATURES ORIGIN

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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="Locusid:84174"

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SPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLEGKDIFLEVTVQRTPLNWK
                                                                                                                                                                                                   be found
                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 88 Row: a Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422.
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// note="SH3; Region: SH3 domain. SH3 (Src homology 3)
domains are often indicative of a protein involved in
signal transduction related to cytoskeletal organization.
First described in the Src cytoplasmic tyrosine kinase.
/db xref="CDD:pfam00018"
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/note="SH2; Region: SH2 domain"
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88.4%; Score 1046; Di
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rassal to 2538)

Rausberg R.L. Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.F., Zeeberg, B., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,

Diatchenko, L., Marusha, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulkk, S.W.,

Villahon, D.K., Walny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffaad, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Botterfield, Y.S., Krzywinski, M.T., Swalka, U., Smailus, D.E.,

Butterfield, Y.S., Rzzywinski, M.T., Skalka, U., Smailus, D.E.,

Butterfield, Y.S., Rzzywinski, M.T., Skalka, U., Smailus, D.E.,

Schnerztion and initial analysis of more than 15,000 full-length
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2538 bp mRNA linear PRI 07-OCT-2003
Homo sapiens Src-like-adaptor 2, transcript variant 1, mRNA (cDNA
COUR MGC:49845 IMAGE:4429896), complete cds.
                                                                                    960
918 ACTCCAGGCCCTGGTGGCCATTACTCTGAGCTGGCGGATGACATCTGTGCTGCCTACTCAA 977
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Direct Submission
Submission
Submitted (33-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                       901 ACTCCAGGCCCTGGTGGACCATTACTCTGAGGTGGAGGATGACATCTGCTGCCTACTCAA
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Contact: MGC help desk
Email: cgapbe.r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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22388257
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

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1116 GTCTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTGGATG 1175
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Mcglade,J.C. and Loreto,M.P.
Adapter gene
Adapter WO 0242452-A 4 30-MAY-2002;
The Hospital for Sick Children (CA)
Location/Qualifiers
1. 786
                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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PAT 27-SEP-2002

linear

DNA

AX511153 786 bp Sequence 4 from Patent W00242452. AX511153 GI:23392046

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5 AXS11153 LOCUS Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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878 TCACCGCGCTCACCTTCCCCTCCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCG 937
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/db_xref="taxon:9606"
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SPRLTFPSLQALVPHYSELADDICCLLKEPCYLQRAGFLPGKDIPLPVTVQRTPLNWK
ELDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Cloning of an inhibitor of antigen-receptor signaling by a retroviral-based functional screen Patent: Wo 02055707, A. 18-JUL-2002;
Rigel Pharmaceuticals, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
                                                                   AX572845 786 bp Sequence 1 from Patent WO02055707.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Drimates; Catarrhini; Hominidae; Homo.
The Drace of 1 to 786)
Lorect, M.P. and McGlade, C.J.
Cloning and characterization of human Src-like adaptor protein 2 and a novel splice isoform, SLAP-2-v
Chocogene 22 (2), 266-273 (2003)
L 257895
E 2 (bases 1 to 786)
L 257895
E 2 (bases 1 to 786)
Lorect, M.P. and McGlade, C.J.
Direct Submission
L Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont MSG 1X8, Canada irce
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/dcpAbLLLLPGNPGGAPLIRESQTRRGSYSLSVRLSRPASWDRIRHYRLHCLDNGWLYI
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Homo sapiens Src-like adaptor protein-2 mRNA, complete cds.
AF290985
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481 TCACCGCGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCG 540
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PAYAN, D.G., Mancebo, H.S.Y. and Mu, J. Funibitor of Antigen Receptor Signaling JOURNAL JOEN, Med. 194 (9), 1263-1276 (2001) WEDLINE 215:3259 REPERENCE Loses 1 to 786) AUTHORS Holland, S.J., Nendenhall, M.K., Zhou, X., Spencer, C., Pardo, J., Mancebo, H.S.Y. and Mu, J. TITLE JU, A.C., Sheng, M., Mancebo, H.S.Y. and Mu, J. TITLE JOURNAL JOURNAL Location/Qualifiers Source Location/Qualifiers Location/Qualifiers Source Location/Qualifiers Location/Qualifiers Location/Qualifiers Source Location/Qualifiers Location/Qualifie	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 785; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Assandarcreconconcancentereconacted accordance and accordance of the conservative 0; Arcschafter of the conservative 0; Mismatches 1; Indels 0; Gaps 0; Assandarcreconconcancentereconacted accordance accordance of the conservative 0; Assandarcreconscentrancentereconacted accordance accordance of the conservation of the conser
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Score 735; DB 9; Length 2415;
Pred. No. 0;
; Mismatches 1; Indels C
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nt WO03039443.
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PAT 27-SEP-2002

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AF290986 137 bp mRNA linear PRI 21-JAN-2003 Homo sapiens Src-like adaptor protein-2 splice isoform mRNA, complete cds, alternatively spliced.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Adapter gene
Pacent: WO 0242452-A 6 30-MAY-2002;
The Hospital for Sick Children (CA)
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S., Dugas, M., Eils, R., Brors, B. and Mergenthaler, S.

Novel genetic markers for leukemias
Patent: WO 03039443-A 3014 15-MAY-2003;

Beutsches Krebsforschungszentrum (DB); Haferlach, Torsten, PD Dr. Dr. (DB); Schoch, Claudia (DE); Kern, Wolfgang (DB)
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                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1. .2788
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Matches 784; Conservative
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878 TCACCGCGCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAG 931
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HTG; NDRG1; SH2 domain
Homo sapiens (human)
Homo sapiens
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AGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSRE
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SPRLTFPSLQALVDHYSEGWPAPWQGYTPTCDCAEDTTQLERAGQLPPVF"
                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 737)
Loreto,M.P. and McGlade,C.J.

Loreto,M.P. and McGlade,C.J.

Direct Submission

Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont MSG 1X8, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AGGGAGAAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATC 360
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                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                 1 (bases 1 to 737)
Loreto, M.P. and McGlade, C.J.
Cloning and characterization of human Src-like adaptor protein 2
and a novel splice isoform, SLAP-2-v
Oncogene 22 (2), 266-273 (2003)
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product="Suc-like adaptor protein-2 splice isoform"
/protein id="AAL38198.1"
/db_xref="GI:17351923"
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99.8%; Pred. No. 1.9e-268;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="SLAP-2-v"
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                                                                   Homo sapiens (human)
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AF290986
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                                                                                              ORGANISM
                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
ACCESSION
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PUBMED
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JOURNAL
                  VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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Direct Submission

Direct Submission

Direct Submission

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

On Aug 7, 2000 this sequence version replaced gi:6425549.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission;

corresponding to the overlapping clone, as we submit sequences with

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp., WORNPEP; Information

on the WORNPEP database can be found at

thtp://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 20, constructed by the Sanger Centre Chromosome 20

Mapping Group: Further information can be found at

http://www.sanger.ac.uk/HGP/Chr20

Mapping Group: Further information can be found at

http://www.sanger.ac.uk/HGP/Chr20

Mapping Group: Further information can be found at

the true right end of clone RP3-460AB is at 66741 in this sequence.

The true right end of clone RP3-460AB is at 5041 in this sequence.

The true right end of clone RP3-460AB is at 500 in this sequence.

The true right end of clone RP3-460AB is at 500 in this sequence.

The true right end of clone RP3-460AB is at 500 in this sequence.

The true right end of clone RP3-460AB is at 500 in this sequence.

The true right end of clone RP3-460AB is at 500 in this sequence.

The true right was made to resolve all sequencing problems, such as compressions and repeate, all regions were ceither double-stranded or sequence was finished as follows were covered by the quality data (i.e., phred quality versemble was confirmed by the group of pieter de Jong Por
                                                                                                                                                        Human DNA sequence from clone RP3-460d8 on chromosome 20q11.21-11.23 Contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, ESTS, STSs and GSSs, ALO31662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
481 TCACCGCGCCTCACCTTCCCCTCACTCCTGGTGGACCATTACTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:B45150"
complement(240. .7128)
/gene="dJ97781.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP3-460J8"
/clone lib="RPCI-3"
complement (50. .544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/db_xref="GOA:QUIGN2"

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/db_xref="GOA:QUIGN2"

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GIGVGAGAYILSRPALNHPELVEGTVLINVDPCAKGWIDMABKLSGLTTNVVDIILA

HHFGGELGANLDLIQTYRMHIAQDINGDNLQLFANSYNGRRDEIFSFRILGENFREAF

KTLKGSTLLVVGDNSFAVERAVVEGNSRLNPINTTLLKVADCGGLPQVVQPGKLTTRAFY

YFLQGAGGYIPVVQLSHLSTESVPSANSTRLARSRTHSTSSSIGSGESPFSRSVTSNQS
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                                                                                                         downstream regulated (NDRG1)
match: proteins: Sw.062433 Sw.092597 Tr.0922L9 Sw.P97862"
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              32039. 32142,37091. 37147,46566. 46652,48268. 48328,50163. 50225,53242. 53362,54429. >54534)
/gene="dJ469A13.3"
/note="novel protein (FLJ13556) similar to N-myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
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note="TIGGER2 repeat: matches 2541. .2714 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9738. .60495
note="TIGGER2 repeat: matches 1780. .2541 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCIAGAGCICCAAGGACCCCACGCCIGIGICTCTGIGACAGAGCICAAAGGGCCCTGGG
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Note="24 copies 2 mer ta 79% conserved"

Note="74 copies 2 mer ta 79% conserved"

Note="WERS2C repeat: matches 1. .127% of consensus"

17899. 48470

Note="match: GSS: Em:AQ672417"

1931. 49480

Note="match: GSS: Em:AQ672417"

19321. 53120
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14313. 34420
note="W1" repeat: matches 1. .109 of consensus"
14505. 34560
note="28 copies 2 mer ta 78% conserved"
                                                                                                                                                                           /evidence=not_experimental
/product="dJ460J8.1 (continued from dJ469Al3.3
Em:AL132768)"
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/note="MER11C repeat: matches 1. .1071 of
62547. .63174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="73 copies 2 mer at 83% conserved"
complement(58930. .59281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (57696. .58013)
/note="match: STS: Em:G07632 Em:G07634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (24246. .24780)
/gene="d469413.3"
/note="match: GSS: Em:AQS92789"
complement (27980. .28556)
/gene="dJ469A13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match: GSS: Em:AQ310681"
7509. .57838
note="match: STS: Em:G07504"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:AQ314824
match: STS: Em:G55853"
54054. .54477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: STS: Em:G04621"
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                                                                                                                                                                                                                                             /protein_id="CAB65625.1"
/db_xref="GI:6687781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGTQESCESPDVLDRHQTMEVSC'
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Best Local Similarity 100.C
Matches 354; Conservative
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join(19202 . 1945).2210. .22282,26087. .26127,30796. .30847)
/noce="match: STS: Em:G23762"
complement (join(19270 . 19451,20551. .20589,22110. .22161,
22247. .22282,26087. .26134,30796. .30847,30986. .31051,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (<17523. 19451,20551. 20589,22110. .22161,
22247. .22282,26087. .26134,30796. .30847,30986. .31051,
27393. .32142,37091. .37147,46566. .46522,48268. .48328,
50163. .50225,53342. .53362,54429. .>54534))
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/b_xref="syliss-prOT:Q9H6G3"
/translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTWBAERSKATAVALGSFP
AGGPAELSIRLGEPLITIVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: ESTs: Em:AA718726 Em:AA039000 Em:AW003952 Em:W89263
Em:AA325826 Em:AI230982 Em:AA162360 Em:AA445016
Em:AV002395 Em:TB5147 Em:AI786615 Em:AA11437 Em:AI004026
Em:T98705 Em:AI786673 Em:AI181197 Em:AA764653 Em:AA316771
                                            'product="dd146038.2 (novel protein tyrosine kinase with
src homology 2 (SH2) domain )"
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/product="dJ46018.2 (novel protein tyrosine kinase with
Src homology 2 (GH2) domain )"
Sprotein id="CAC44645.1"
/ab_ref="dI:1520830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: cDNAs: Em:AB033922 Em:U52073 Em:D87953
Em:X92845 Em:AF004162 Em:U60593 Em:AF045564 Em:AB033921
Em:AF159092 Em:AF147402 Em:M59814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .785 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .422 of consensus'
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100te="MERZIB repeat: matches 1. .355 of consensus"

20mplement(17516)

17519. .17686

7.00te="match: GSS: Em:AZ067993"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Product="dJ460J8.1 (continued from dJ469A13.3 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375. 2402
note="14 copies 2 mer ta 100% conserved"
    :omplement(join(<240. .339,6995. .7128))
gene="dJ977B1.1"</pre>
                                                                                                                                    /evidence=not experimental
complement(join(<240. .339,6995. .7085))
gene="dJ977B1.1"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0615. .10640
/note="13 copies 2 mer tt 92% conserved"
13593. .13961
/note="MER21B repeat: matches 422. .785'
14248. .14297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copies 2 mer ag 93% conserved"
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4594. .14614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2783. .3155

/note="match: GSS: Em:AQ807191"

complement(6983. .7482)

/note="match: GSS: Em:AQ556467"

complement(6985. .7492)

/note="match: GSS: Em:AQ556478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486. .7925
Thote="match: STS: Em:HS427J1S"
0615. .10640
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complement(17542, .17547)
gene="dJ469A13.3"
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complement (17542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                536. .565
/note="15
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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------- Froject Information
center project hame: L7115
Center clone name: 712_N_14
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NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 125577 bases at least Q40 consensus quality: 135703 bases at least Q30 Consensus quality: 135703 bases at least Q30 Insert size: 182000; agarose-fp Insert size: 182200; agarose-fp Quality coverage: 2.6 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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1110 90855: contig of 3746 bp in length 90855: contig of 3746 bp in length 90855: contig of 3746 bp in length 90855: gap of 100 bp in length 90856: gap of 100 bp in length 908620: contig of 5565 bp in length 90821: contig of 5701 bp in length 102421: gap of 100 bp in length 102421: gap of 100 bp in length 108423: gap of 100 bp in length 116789: gap of 100 bp in length 116789: gap of 100 bp in length 125364: contig of 8475 bp in length 13554: contig of 100 bp in length 1355 13654: gap of 100 bp in length 1355 13654; gap of 100 bp in length 1355 13634; gap of 100 bp in length 1355 146833: contig of 9379 bp in length.
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Direct Submission

Submitted (19-UTL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. Email enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Jul 28, 2000 this sequence version replaced gi:5924017.

During sequence assembly data is comparated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNDEP; Information
on the WORNDEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99805 CCTTCCCTCCTGGCTGGCTGTGCTTGGGAGGGTTCCCCAGTCCAGAATCCCTAAGGAG 99864
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Human DNA sequence from clone RES-977B1 on chromosome 20 Contains BSTS, STSS, GSSs and three putative CpG islands. Contains the 3' end of the gene for a novel protein tyrosine kinase, a heterogeneous nuclear ribonucleoprotein A3 pseudogene, the gene for three isoforms of a novel protein similar to putative the second of a novel protein final of putative threating protein, the TGTP2 gene for TGF(beta)-induced transcription factor 2 with two isoforms, the MYRL2 gene for myosin regulatory light chain 2 (smooth muscle isoform), the 3' end of the gene KIAA0964 (ortholog frat RSD-95/SAP90-associated protein 4) with two isoforms and a novel gene, complete sequence.
                                                                                                                                                                                                                                                                          99745 AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGGCCCTGGG 99804
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100045 GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCA 100098
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HTG; CpG island; heterogenous ribonucleoprotein; KIAA0964; my regulatory light chain; MYRL2; RAB5-interacting protein; SH2 domain; TGIF2; transcription factor; tyrosine kinase. Homo sapiens (human)
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0
                                                                                       Query Match 29.9%; Score 354; DB 2; Length 145833; Best Local Similarity 100.0%; Pred. No. 1.1e-193; Matches 354; Conservative 0; Mismatches 0; Indels 0;
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55036._.59553
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HSDJ977B1/c
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KEYWORDS
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Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-977B1 The true left end of clone RP3-460/B is at 63245 in this sequence. The true right end of clone RP3-18019 is at 63245 in this sequence. This sequence was finished as follows unless otherwise noted all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-977B1 is from the library RPCIS constructed by the group of Pieter de Jong. For further
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34968. .35059. 35659. .36724,37531. .39331)
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/note="LIMC/D repeat: matches 5432. .5528 of consensus"
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http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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1. .145068
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568. .875
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KENNISEBULGKVLSAVGSAQLIMSOKROOPRGILCBONINPDANPRPTAQDLAGFWDI.
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TDSDTQDANDSSCKSSERSLPDCTPHPNSISIDAGPRQAPKIAQIKRNLSYGDNSDPA
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DKASDASDKQRQEARKRLLAAKRAASVRQNSATESADSIEIYVPEAQTRL"
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Tr:014490 Tr:P97836 Tr:P97837 Tr:054773 Tr:P97841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                continues in dJ996C2 (AL445705) and bK2182L9 (AL390374) match: proteins: Tr:Q9Y2H0" /codon start=3
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Thote="MIX Tepeat: matches 11. .236 of consensus"
11767. 11782
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126034 CTACAGGATCCACTGACAATGGCTGGCTGTACATCTCACCGCGCCTCACCTCCC 125975 Query Match 12.8%; Score 152; DB 9; Length 145068; Best Local Similarity 100.0%; Pred. No. 3e-76; Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 838 CTACAGGATCCACTGCCTTGACAATGGCTGGTGTACATCTCACCGCGCCTCACCTTCCC 897 778 AGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCTGCATCGGACCGGATCAGACA 837 g ò

898 CTCACTCCAGGCCCTGGTGGACCATTACTCTG 929

Search completed: February 20, 2004, 07:24:47 Job time : 4588 secs

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February 20, 2004, 01:41:55 ; Search time 503 Seconds (without alignments) 9991.289 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aak28314 Human bon Aak02872 Human bra Abs27912 Human liv Aai02797 Probe #27 Human mod Human Src Human ORF Human ORF Mouse MAR DNA encod DNA encod Human ORF Human ORF DNA encod DNA encod Probe #29 Human bre Abk61465 Human cDN Aad43980 Human Src Probe #28 Human cod Probe #28 Description Aa144090 Abq74343 Abq98669 Abq99151 Aba54580 SUMMARIES AAK02872 ABS27912 AAI02797 Query Match Length DB 483 468 405 401 348 Result

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Abs02823	Aai14520	Abs04499	Aa;22119	Aba67198	474	Aba49284	Aba34292	Aak41374	Aak15640	Abs40966	Aai07818	Abs15380	Aa144087	Aad43983	Abk61506	Aa144100	Aa144098	Aa144099	Aa144097	Abk61507	Aax55277	
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ALIGNMENTS

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Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; call signal processing disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kekuda R, Shimkets RA;
er JN, Yang R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grosse WM, Hart M, Kekud
Tomlinson JE, Topper JN,
                                                                                                             Human cDNA encoding protein NOV13.
                           ABK61465 standard; cDNA; 1183 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 98; 263pp; English
                                                                                                                                                                                                                                                                                                                                                              25-AUG-2000; 2000US-0228191P.
08-FEB-2001; 2001US-0267300P.
20-FEB-2001; 2001US-026951P.
20-MAR-2001; 2001US-0277337P.
                                                                                                                                                                                                                                                                                                                                    27-AUG-2001; 2001WO-US026510.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP. (CORT-) COR THERAPEUTICS INC.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burgess CE, Conley PB,
Spytek KA, Szekeres ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-280937/32.
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                                                                                                                                                                                                                                                                                WO200216599-A2.
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                18-JUN-2002
                                                                                                                                                                                                                                                                                                          28-FEB-2002.
                                                      ABK61465;
RESULT 1
ABK61465
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The invention relates to an isolated polypeptide (NOVX) a mature form of

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NOVX, a NOVX variant (differing by no more than 15%), the nucleotide encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14, 254, 155, 164, and 165. The NOVX polypeptide, nucleic acid encoding it and antibody against it, rae useful for treating or preventing (e.g. by gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy, theresolves a NOVX-associated disorder in humans, e.g. cardiomyopathy, and antibody against it, are useful for cell signal processing and metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide are and and polypeptide of and mucleic acids are also useful for determining the presence of predisposition to the diseases. The NOVX nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for activity, e.g. cancers (e.g. adenocazcinoma, lymphoma, prostete cancer or uterus cancers), immune response, graft-versus-hort disease, acquired immunodeficiarcy syndrome (AIDS), asthma, tronfor's disease, acquired congenital heart defects, multiple sclerosis, inflammation or Albright bereditary osteodystrophy and many other diseases listed in the specialization. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, or treating the conditions. This is also useful in detection assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present cancer or encodes a NOVX protein
              $$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 U; 0 Other;

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                                                                                               Gaps
                                                                                               0
    Score 1183; DB 6; Length 1183;
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                                           ; Pred. No. 0;
0; Mismatches
    100.08;
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Matches 1183; Conservative (
Query Match
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                                                               GTTGTTACCTGGGAACCCTGGAGGGCCTTCCTCATCCGGGAGAGCCAGACCAGGAGAGA
                                                                                               GTTGTTACCTGGAACCCTGGAGGGGCCTTCCTCATCCGGGAGAGCCAGACCAGGAGAGG
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CAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAGAAAGCAGAGAACTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Src-Like Adapter Protein-2 (hSLAP-2) cDNA.
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/product= "Human SLAP-2"
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The invention relates to a substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-C). The invention is useful for trearing an immune disorder involving hyperactivity of B- or T-1 ymphocytes in a manmal. The invention is useful for scenarior of the interaction of hyperactivity of B- or T-1 ymphocytes in a manmal. The invention is useful for scenarior of the interaction of histappe 2 with callular signalling compounds, for diagnosing, treating or preventing diseases or disorders associated with aberrant or uncontrolled collular signal transduction, for determining those cellular signalling molecules which associate with hSLAP-2 and which provide critical signals for cell activation, and as effectors in methods to affect T-cell activation, and as effectors in methods to affect T-cell activation. The invention is useful in screening assays to identity and activation. The invention is useful in screening assays to identity and cetter candidate bioactive agents that modulate hSLAP-2 bioactivity, for potential use to treat autoimmune diseases which may be caused by hyperactivated B cells, as well as to treat diseases which may be caused to hyperactivated T cells, in addition to other immune system related conditions, diseases, or disorders, T-cell and B-cell neoplasms, of theorative colitis), allergies, particularly those involving and ulcerative colitis, autoimmune diseases such as systemic lupus eryhmm actual respiratory distress syndrome, and chronic obstructive pulmonary disorder, tissue/ organizatory distress syndrome, and cancer. The invention is useful in gene therapy. The present sequence is human SLAP-2 cDNA
                                                                                                      Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic intervention in immunological and inflammatory disorders and cancer.
                                                                                                                                                                                                                         Claim 2; Fig 1; 85pp; English.
                      WPI; 2002-463632/49.
P-PSDB; AAE26357.
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Sequence 2567 BP; 611 A; 741 C; 666 G; 549 T; 0 U; 0 Other;

0; Gaps 95.7%; Score 1132; DB 6; Length 2567; 99.9%; Pred. No. 0; 0; Mismatches 1; Indels Query Match Best Local Similarity 99.9° Matches 1182; Conservative 1 AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGGCCCTGGG 60

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61 CCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGTCCAGAATCCCTAAGGAG 120 197 240 300 317 78 cerrecerecerederedecrerecerredecadeserreceasereceradareceradas 137 257 18 AGCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGGCCCTGGG 138 cardedecaderrearcerregreracaacrecreacrecadacadarecreaderrecreacer 181 ACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTG 198 ACCCAAACCAACATAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTGGGTG TCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCCA Toctraggaccaaggacaccagactrocagaaggcccccaaaggcccraaagcargroca 258 셤 ें dd g

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1021 GACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTGGAÇAGCTCCCTCCTGTGTTTTCTGA 1080 GGAGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGT 1020 978 geadddchdrafachaeadaddchaeddchachaedahahachachachar 1037 1081 AGCTGCCACAGGGGAGGTCTCTTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTCTA 1140 1098 AGCTGCCACAGGGGAGGAGTCTCTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTCTA 1157 901 ACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCTACTCAA 960 CICITACICICIGICAGICCGCCICAGCCGCCCIGCAICCIGGGACCGGAICAGACACIA 840 858 CAGGATCCACTGCCTTGACAATGGCTGGGCGGATCTCACCCTCACCTTCCCCTC 917 Human, gene; ss; gene therapy; modulator of antigen receptor signalling; MARS; tumour suppressor gene; Sor-like adaptor protein; 5LAP; MARS; tumour suppressor gene; Sor-like adaptor protein; 5LAP; myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer. Human modulator of antigen receptor signalling protein coding sequence. crcrracrcrerereagreegeercageegeereearceragaeegaeare CAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCGCGCCCTCACCTTCCCCTC 918 ACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCTACTCAA 1158 CATCAGCCTGAATGACGAGGCTGTCTTTTGGATGATGCCTAG 1200 1141 CATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG 1183 Location/Qualifiers AAL44089 standard; cDNA; 786 BP. 03-OCT-2002 (first entry) ι¢ 1. .786 /*tag= Homo sapiens. 841 196 781 RESULT 3 AAL44089 g 엄 à 臼 8 a 임 셤 ò 쉱 BXLLLLXSXEEXEXSXELLL 8 ⋩ à Š

/product= "Human MARS protein"

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421 AAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCAT 480

378 credaricaricricricacricricricricacidadeacaricaceangeag

AAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCAT 497

377 420

GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC 360

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318 GCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCC CTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGAAGTCTGCCCAGCAGAAG

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678 CAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAAAAGCAGAGAACTGCT 737

GTTGTTACCTGGGAACCCTGGAGGGCCTTCCTCATCCGGGAGAGAGCCAGACCAGGAGAGG

618 GTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGGTATAACATCCCCAGCGTCCACGTGGC 677

GTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGTATAACATCCCCAGCGTCCACGTGGG

558 GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGACTG

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GGAAGCAGAGAAGCAAGGCCACAGCCGTGGCCAGGTTTCCCGGCAGGTGGCCC 540 498 GGAAGCAGAGAAGGAAGGCCACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCCC 557 GGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTGAGGATGGAGGACTG 977

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The present sequence encodes the human Src-like inhibitory molecule (SLIM) protein (I). The present invention describes a SLIM protein comprising an N-terminal sequence, an N-terminal SH2 domain, and an N-terminal SH3 domain which can bind to Cbl, or comprising an N-terminal myristylation sequence and an N-terminal SH2 domain which is unable to bind to Cbl. (I) has antiinflammatory, immunosuppressive and
                                                                                                                                                                      GACAGCTCCCTCCTGTTTTCTGAAGCTGCCACAGAGAGGAGTCTCTTCTCAGTGAGGGT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, Src-like inhibitory molecule, SLIM, Src-like adapter protein, SLAP; inhibitor; antiinflammatory; immunosuppressive; anti-HIV; modulator; lymphocyte; CD; gene therapy; immunodeficiency disorder, acquired immune deficiency syndrome; ADB; acute inflammatory disorder; chronic inflammatory disorder; autoimmune disorder; transplant rejection;
GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTG
                                                                                                                         601 GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGGGCTG
                                                                                                                                                                                                                   661 GACAGCICCCICCTGTTTTCTGAAGCTGCCACAGGGGAGGGAGTCTCTTCTCAGTGAGGGT
                                                                                                                                                                                                                                                                     CTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTTGGATGAT
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Sheng N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New src-like inhibitory molecule protein, useful for treating immunodeficiency disorders and inflammatory disorders, comprises N-terminal myristylation sequence, SH2 domain and/or SH3 domain.
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Shen M, Liao XC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (WARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Sor-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myelofd malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a human MARS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                        New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
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                                                                                                                                                                      (HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 75; 110pp; English.
                                                                                                                         27-NOV-2000; 2000CA-02324663.
                                                                            26-NOV-2001; 2001WO-CA001662.
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                                                                                                                                                                                                                      Mcglade JC, Loreto MP;
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activation, and of ubiquitination of a Cbl target protein, and in gene activation, and of ubiquitination of a Cbl target protein, and in gene thereby. (I) is useful for screening a bloactive agent capable of binding to SIIM. (I) is also useful for screening a bloactive agent capable of modulating SIIM binding. (I) or its fragments is useful in the study or in the treatment of conditions which involves this function or dysregulation of SIIM protein activity, i.e. to diagnose, treat or prevent SIIM associated disorders. (I) or the polynucleotide encoding it (II) is useful for modulating leukocyte and/or platelet activation, for modulating antigen receptor-induced signalling and activation in leukocyte and/or mast cells. (I) or leukocyte and/or platelets and for modulating antigen receptor-induced signalling antigen receptor-induced signalling antigen for modulating the basal activity of lymphocytes. (I) or is also useful for modulating the basal activity of lymphocytes. (I) or is also useful in the treatment of immunodeficiency disorders, such as acquired immunodeficiency syndrome (AIDS), for the prevention and treatment of acute inflammatory disorders, choic inflammatory disorders, autoimmune disorder and transplant rejection
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                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0;
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Matches 785; Conservative
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The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ99194-ABQ99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HVVBC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atheroscierotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood cardiovascular disease, inflammatory disorders. Note: The sequence data for this patent did not form at the printed specification, but was obtained in electronic format directly from the USPTO web site at
New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human unbilical veh endothellal cell; HUVEC; atheroscierotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                           ABQ98670 standard; DNA; 763 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORF477 coding sequence.
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(MEHR/) MEHRABAN F.
(CONL/) CONLEY P B.
(TOPP/) TOPPER J N.
                                                                                                                                                                                     781 GCCTAG 786
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177 AGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGTTCTG
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RESULT 6
AAC77202 standard; CDNA; 837 BP.
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AAC77202 standard; CDNA; 837 BP.
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Human ORFX ORF2757 polymucleotide sequence SEQ ID NO:5513.
XX
Human; Open reading frame; ORFX; detection; cytostatic; hepatotropic; XX
Human; Open reading frame; ORFX; detection; cytostatic; hepatotropic; XX
Human; Open reading frame; ORFX; detection; cytostatic; hepatotropic; XX
Human; Open reading frame; ORFX; detection; cytostatic; hepatotropic; XX
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
cardiant; thrombolytic; coaquiant; vasotropic; antibabetic; hypotensive;
cardiant; thrombolytic; coaquiant; vasotropic; antibabetic; hypotensive;
cardiant; thrombolytic; coaquiant; vasotropic; antibabetic; hypotensive;
cardiant; thrombolytic; coaquiant; vasotropic; antibabetic; hypotensive;
cardiant; thrombolytic; cardiant; antibacterial;
antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
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conditions. To inhibit thrombosis; and as contraceptive
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allergy, aplastic anaemia, nocturnal haemoglobinuria; burn; wound, bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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                                                                                                                                                                                                                                                       31-MAR-2000; 2000WO-US008621.
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02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-012728P.

30-MAR-2000; 2000US-00540763.
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                                                                                                                                                      WO200058473-A2.
                                                                                                      Homo sapiens.
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979 GAGGGCTGGCCCGCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACC 1038
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                                                                                                                                                                                                                                                                                                                                          363 CCGCCTCAGCCGCCCTGCATCCTGGGATCAGAACACTACAGGATCCAGCCTTGA 422
                                                                                                                                                                                                                                                                                                                                                                                                                           859 CAATGGCTGGCTGTACATCTCACCGCCCTCACCTTCCCCTCACTCCAGGCCCTGGTGGA 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482
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                                                  recadedecerrecterreces and accade accade accade accretion encores and accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade accade acc
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                                                                                                                                   The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibite structural and sequence similarity to the Sor-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a mouse MARS protein
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                    New isolated modulator of antigen receptor signaling protein or its
                                        fragment, useful for treating malignant disorders such as myeloid
malignancies, autoimmune disorders and myeloproliferative disorders.
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40.8%; Score 483; DB 6; L
Best Local Similarity 99.8%; Pred. No. 8.9e-218;
Matches 533; Conservative 0; Mismatches 1;
                                                                                                 Claim 9; Page 77; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human coding sequences (ABG99268-ABG99608) and proteins (ABF64682-ABF65022). The sequences are useful in the research methods. The polynucleorides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed sequence tags (BST8) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or manufacture of bio-pharmaceuticals or the development of bio-sensors. The biological activity, e.g. haematopolatic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, or cancer. The polynucleotide sequences of the invention were assembled from ESTS isolated mainly by sequencing by hybridisation, and in some cases, sequences obtained from one or more public databases. Note: The sequence of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, or sequences of the printed specification, or sequences of the printed specification, or sequences of the printed formatic format directly from WIPO at
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immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiaflergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 TGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGAA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.6%; Score 468; DB 6; Length 1413; 99.6%; Pred. No. 1e-210; ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                           iu C, Zhou P, Asundi V
Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 107; 394pp; English.
                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                     16-NOV-2001; 2001WO-US042950.
                                                                                                                                                                                                                                                        17-NOV-2000; 2000US-00714936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                               Yang Y,
                                                                                                                                                                                                                                                                                                                               Goodrich RW,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590824/63.
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                                                                                                                                                                                                                                                                                          HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABP64788
                                                                                                                                                                                                                                                                                                                                               Xue AJ,
                                                                                                                                               WO200259260-A2.
                                                                                                               Homo sapiens.
                                                                                                                                                                                      01-AUG-2002.
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121 AGGGACCTGTGACCATGGAAGCAGAGAAAGCAAGGCCACAGAGCCGTGGCCCTGGGCACAGTT 180
                                                                                                                                                                                                                                                                                                                                                                                             704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 CCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GCCAGACCAGGAGAGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGGG 480
                                                                              525 TCCCGGCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGGAGCCATTGACCATCGTCT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
                                                                                                                                                       181 TCCCGGCAGGTGGCCCCGGCCGAGCTGTCGCTGAGACTCGGGGGAGCCATTGACCATCGTCT
                                                                                                                                                                                                                                 585 CTGAGGATGGAGACTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTATAACATCC
                                                                                                                                                                                                                                                                                                           241 cheaddandandachdandandandrichtaadroncaddadadananaacance
                                                                                                                                                                                                                                                                                                                                                                                             645 CCAGCGTCCACGTGGGCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 AAGCAGAACTGCTGTTGTTACCTGGGAACCCTTGGAGGGCCTTCCTCATCCGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AAGCAGAGGAACTGCTGTTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 GCCAGACCAGGAGAGGCTCTTACTCTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #10552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                885 GCCTCACCTTCCCCTCACTCCAGGCCCTGG 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS74748 standard; cDNA; 603 BP
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABG10561
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in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to tradt disease states involving (III). (II) is useful for generating antibodies against it, detecting or quantitating apripated in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAAS9454 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print
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Sequence 603 BP; 124 A; 189 C; 164 G; 126 T; 0 U; 0 Other;

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1079 GAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTC 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 GGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCTGCATCCTGGGACCGGATCAGACAC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
                                                                                               779 GGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGGGATCAGACAC 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 GAAGCTGCCACAGGGGAGGAGTCTCTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTC 558
                                                                                                                                                                                               839 TACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCGCGCCTCACCTTCCCC 898
                                                                                                                                                                                                                                            259 TACAGGATCCACTGCCTTGACAATGGCTGGGTGTACATCTCACCGCGCCTCACCTTCCCC 318
                                                                                                                                                                                                                                                                                         899 TCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTC 958
                                                                                                                                                                                                                                                                                                                                               TCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCCTACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      379 AAGGAGCCCTGTGTCCTGCAGAGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCT
                                                     0; Gaps
Query Match 34.2%; Score 405; DB 5; Length 603; Best Local Similarity 100.0%; Pred. No. 6.3e-181; Matches 405; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1139 TACATCAGCCTGAATGACGAGGCTGTCTTTTGGATGATGCCTAG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 TACATCAGCCTGAATGACGAGGCTGTCTTTTGGATGATGCTAG 603
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                               DNA encoding novel human diagnostic protein #10554.
                     AAS74750 standard; cDNA; 2049 BP
                                                            (first entry)
                                                                                                                                                      WO200175067-A2,
                                                                                                                                   Homo sapiens.
                                                             13-FEB-2002
                                                                                                                                                                          11-OCT-2001
                                        AAS74750;
RESULT 10
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30-MAR-2001; 2001WO-US008631.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PGR) primers, and for thromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) at useful in gene therapy techniques to restore normal cutivity of (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and on the printed sequences and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS9464 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WND at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1042 GACCATGGAAGCAGAGGAAGCAAAGGCAACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGG 1101
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                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2049 BP; 479 A; 573 C; 551 G; 443 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 10554; 103pp; English.
                   31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                (HYSE-) HYSEO INC.
                                                                                                                                                                                                                            P-PSDB; ABG10563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary, Antinfilammatory, gene therapy, human, ORFX, atherogenic, platelet, human umbilical vein endothellal cell, HUVEC, atherosclerotic plaque, cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood coagulation disorder, inflammatory disorder, ds.
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GAGAGGCTCTTACTCTCTGTCAGTCCGCCTCA 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 951; 78pp; English.
                                                                                                                                                                                                                       ABQ98669 standard, DNA; 444 BP
                                                                                                                                                                                                                                                                                                                                                                                                             Human ORF476 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2001; 2001US-00867550.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disease.
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P-PSDB; ABP64106.
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(MEHR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
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                                                                                                                                                                                                                                                                                                                                               04-NOV-2002
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   775
                                                                                                                                                                                                                                                                                     AB098669;
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The present invention relates to novel human ORFX polypeptides and their coding sequences (ABF63611-ABF64681 and AB696194-AB099267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HVDEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherogenical plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological
CCAGAGCATGCGTCTCCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCCC 361
                                        61 CCAGAGCATGCGTCTCAGCAGAGCTGTCTTTCCAAGCCTTTGATGACAAACCAATTTCCC 120
                                                                                  421
                                                                                                                          121 TCGATGATGTGCTTCTGAGTGCTCTGAGGAACAATGGGAAGTCTGCCCAGCAGAAGA 180
                                                                                                                                                                       422 AAAICTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCAIG 481
                                                                                                                                                                                                             181 AAATCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCATG 240
                                                                                                                                                                                                                                                            GAAGCAGAGAGAAGCAAGGCCACAGGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCCCG 541
                                                                                                                                                                                                                                                                                                    241 GAAGCAGAGAAGCAAAGGCCACAGCCGTGGCCCTGGGCAGTTTCCCGGCAGGTGGCCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary, Antiinflammatory, gene therapy, human, ORFX, atherogenic, platelet; human umbilloal vein endothelial cell; HUVEC, atherosclerotic plaque, cancer; cardiovascular disease, allergy, autoimmine disease, wound healing; blood coagulation disorder; inflammatory disorder; ds.
                                                                                  362 TCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGAAGTCTGCCCCAGCAGGAGA
                                                                                                                                                                                                                                                                                                                                               542 GCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAG 589
                                                                                                                                                                                                                                                                                                                                                                      301 GCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conley PB, Topper JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 1915; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ99151 standard; DNA; 875 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORF958 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEAC/) LEACH M D.
(MEHR/) MEHRABAN F.
(CONL/) CONLEY P B.
(TOPP/) TOPPER J N.
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                                                                                                                                                                                                                                                            482
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302
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963 AGCCCTGTGTCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083 CTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTCTACA 1142
condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20020082206
                                                                                                                                                                                                                                            843 GGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACGGCGCCTCACCTCACCTCAC
                                                                                                                                                                                                                                                                                                                      903 TCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGACATCTGCTGCTTACTCAAGG 962
                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AGCCCTGTGTCCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 recaddecerderacarracrerdaderadedaardacarerderaceraceracaada 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 CTGCCACAGGGGAGGAGTCTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTCTACA 301
                                                                                                                                                                                                                                                                       2 GGATCCACHGCCTTGACAATGGCTGGCTGTACATCTCACGGGCCTCACCTCCCCTCAC 61
                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                       Length 875;
                                                                                                                              Sequence 875 BP; 205 A; 259 C; 225 G; 185 T; 0 U; 1 Other;
                                                                                                                                                                   28.8%; Score 341; DB 6; Length 875
100.0%; Pred. No. 1.1e-150;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1143 TCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 TCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #10551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS74747 standard; cDNA; 445 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                             Query Match
Best Local Similarity 100.0°
Matches 341, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tagg for identifying expressed carbivity of (II) is useful in gene therapy techniques to restore normal control of (II) is useful in gene therapy techniques to restore normal control of (II) is useful in gene therapy techniques to restore normal control of (II) or to traat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of supplement. (II) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and anino acid sequences. AASG4197-AASG464 represent novel human diagnostic coding sequences. AASG4197-AASG464 represent novel human diagnostic coding sequences. AASG4197-AASG464 represent did not appear in the printed specification, but was obtained in electronic format directly from WhO at the five the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 CTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGTCCAGAATCCCTA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 CTGGGCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGTCCAAATCCCTA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCTACCCAAACCAACACCCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGAGT-TC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 GAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGCTGAGAGATATC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGTGTCCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACC 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 445 BP; 89 A; 112 C; 143 G; 101 T; 0 U; 0 Other;
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                   Claim 1; SEQ ID NO 10551; 103pp; English.
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Probe #2812 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                            Probe; human; microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312P
                                                                         12-OCT-2001 (first entry)
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                                                                                                                                                                                                    cervical cancer; ss
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                                                                                                                                                                                                                                                        Homo sapiens.
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                              AAI12879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FOR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed continuous. (I) is useful in gene therapy techniques to restore normal ectivity of (II) or to traat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics for genetating desorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the windown of the invention of the confidences.

It p. whop.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708 CAGAGGAACTGCTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAGAGCC 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 GCGTCCACGTGGGCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.9%; Score 141; DB 5; Length 211; Best Local Similarity 99.5%; Pred. No. 3.5e-56; Matches 191; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 211 BP; 50 A; 51 C; 72 G; 38 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 5985; 103pp; English.
                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                               31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG05994
                                              WO200175067-A2.
Homo sapiens.
                                                                                               11-OCT-2001
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989 CCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGACACCACTCAACTGG 1048
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 GAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 CCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGAGACACACCACTCAACTGG 389
                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Helia cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929 GAGCTGGCGGATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1100.0%; Preq. ....
                                                                                                                 Claim 25; SEQ ID NO 2812; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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es 134; Conservative
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AAI12879 standard; DNA; 432 BP.

RESULT 15 AAI12879 ID AAI128

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Perfect score: Scoring table;

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Word size :

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Database :

BG178487 602328305 BG284179 602408226 BQ053486 AGENCOURT

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ALS41041

1201 bp mRNA linear EST 12-MAY-2003
ALS41041 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE00SYK23
S-PRIME, mRNA sequence,
ALS41041
ALS41041.2 GI:30544829
              BG178487
BG0284179
BG0284179
BG023486
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BB619854
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BG388843
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BG282272
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Homo sapiens
                                                                            LOCUS
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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ALS41041
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BQ054265 AGENCOURT
BQ054281 AGENCOURT
                                                  February 20, 2004, 05:08:33; Search time 2929 Seconds (without alignments) 12061.099 Million cell updates/sec
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                         27513289 segs, 14931090276 residues
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                                    OM nucleic - nucleic search, using sw model
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BQ054265
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Gapop_60.0 , Gapext 60.0
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em_gas_rod:*
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em_gas_vrl:*
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Result

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CB657651 OSJNEC13C BE030537 128644 MA AA365070 EST75755 CG869927 XS0853 Sa

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SOURCE
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/note="Vector: pMWSPORT 6, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, the Not I and cloned into the Not I and cloned into Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 TAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCCAGGC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AGAGGATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTGATGACAAACCAATTTCCCTC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 GATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGAAGTCTGCCCAGCAGAAGAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 ATCTCTGCCAAGCCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCATGGA 544
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Faraday Avenue Genoscope sequence ID : CSODE005AF12QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        62.1%; Score 735; DB 9; Length 1201; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0;
0; Mismatches
                                                                                               /organism="Homo sapiens"
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nes 835; Conservative
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/dine="ImAGE:5933542"
/tissue_type="natural killer cells, cell line"
/lab host="im108 (phage-resistant)"
/clome_lib="NIH MGC_106"
/note="Organ: blood; Vector: pCTB7; Site_1: XhoI; Site_2:
RockI; cDNA made by oligo-dT priming blrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II R. (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1to 1002)

8 NIH-MC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

10 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC cloum distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2118 row d column: 23

High quality sequence stop: 670.
                                                                                                                                                                                                                                                                                 BQ052308 1002 bp mRNA linear EST 29-MAR-2002
AGENCOURT_6868571 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933542
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'db_xref="taxon;9606"
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720 TGTTGTTACCTGGGAACCCTGGAGGGGCC 748
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AGENCOURT_6830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936339
BQ054265
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271 IGACCATCGTCTCTGAGGATGGAGACTGGTGGAGGTGCTGTCTGAAGTCTCAGGCAGAG 330
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
1. 986
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JO20 bp mRNA linear EST 29-MAR-2002
S, mRNA sequence.
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into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                       Query Match

48.9%; Score 578; DB 12; Length 986;
Best Local Similarity 99.8%; Pred. No. 1.2e-281;
Matches 628; Conservative 0; Mismatches 1; Indels C
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664

724

us-09-939-853a-74.oli.rst

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/organism="Homo sapiens"
/mol type="mRNA"
/db_Xref="taxon:9606"
/clone='IMAGE:5933772"
/tissue_type="natural killer cells, cell line"
/lab_host="halbs (phage-resistant)"
/lab_host="hilbs (phage-resistant)"
/clone_lib="hilbs (phage-resistant)"
/clone_lib="hilbs (phage-resistant)"
/clone_lib="hilbs (phage-resistant)"
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: blood; Vector: poTB7; Site_1: Site_2:
/note="Organ: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; Vector: blood; V
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AGENCOUNT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772
5., mRNA Fequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1069)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel Mcvicar, DBS/NCI
Tissue Procurement: Dr. Daniel Mcvicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2118 row: n column: 13
High quality sequence stop: 681.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BQ052468.1 GI:19811808
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mRNA"
/db_zref="mRNA"
/db_zref="taxon:9606"
/dlone="INAGB:5936362"
/tissue type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/lone lib="NH MC 106"
/note="Organ: blood; Vector: poTB7; Site 1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript. II RT (Life Technologies). Note: this is a
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                  Email: ogaphs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2155 row: j column: 11
High quality sequence stop: 556.
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Robert Strausberg, Ph.D.
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                 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pcMVSPORT 6 vector. Library was normalized."
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Nath-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Productment: DCTD/DTP
Tissue Productment: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can letuch through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                         Query Match
38.8%; Score 459; DB 13; Length 616;
Best Local Similarity 99.8%; Pred. No. 2.7e-221;
Matches 509; Conservative 0; Mismatches 1; Indels
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 616)
1. (bases 1 to 616)
1. (A.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDbr, Libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9825.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.egi?seq=CSODJ013BF05QP1&cluster=9825.r. Contact
Feng Liang Email: filangelifetech.com/ NRL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
FaradaA Avenue Genoscope sequence ID : CSODJ013BF05QP1.
GCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCATGGAAGCAGA
                                                                                                  GAGAAGCAAGCCACAGCGTGGGCCCTGGGCAGTTTCCCGGGAGGTGGCCCGGCCGAGCT
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/mol_type="markhy"
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/clone="CSODJ013YK10"
/cell_type="JT CELLS (JURKAT CELL LINE) COT 10-NORMAI /cell_line="JINE"
/cell_line="JINE"
/clone="Homo sapiens T CELLS (JURKAT CELL LINE)
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Homo sapiens cDNA clone (BX383606
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BX383606
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PEATURES

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TITLE
JOURNAL
COMMENT
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                                                                                                                  /organism="Homo sapiens"

/mol_type="mRNN"

/db_xref="txxxn:9606"

/db_xref="txxxn:9606"

/clone="type="adenocarcinoma, cell line"

/lab host="HIP RG phage-resistant)"

/lab host="HIP RG phage-resistant)"

/clone lib="NIH MGC 91"

/clone lib="NIH MGC 91"

/clone lib="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
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MENA sequence.

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BG284179.1 GI:13034866

sapiens (human) sapiens

Ношо

VERSION KEYWORDS SOURCE ORGANISM

LOCUS ACCESSION

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 566)

1. (hases 1 to 566)

1. National Institutes of Health, Mammalian Gene Collection (MGC)

1. Unpublished (1999)

1. Contact: Robert Strausberg, Ph.D.

1. Email: cgapbe.refmail.nih.gov

1. Tissue Procurement: DCTD/DPP

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2

Location/Qualifiers
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AGBNCOURT 6822017 NIH_MGC_106 Homo sapiens cDNA clone INAGE:5935253
5., mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="adenocarcinoma, cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4520382"
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BQ053486
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us-09-939-853a-74.oli.rst

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474 TGGTGGACGGTGCTGTCTGAA 494
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Best Local Similarity 100.
Matches 300; Conservative
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/clone lib="NH108 (phage-resistant)"
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ROORI; cDNA made by oligo-dT priming Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                         In (Dazes 1 to 0 78)

NIH-WGC fittp://mgc.nci.nih.gov/.

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: Gapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be thtp://image.llnl.gov l column: 06
High quality sequence stop: 394.

Liocation/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Publisha="Homo sapiens"

// organism="Homo sapiens"
                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 878)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                             Homo sapiens (human)
Homo sapiens
    32053486.1
VERSION
KEYWORDS
SOURCE
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Email: hunquery@sanger.ac.uk
Sanger Centre name: sccd10818.154136A
Homo sapiens EST sequence. This sequence was generated as part of
homo sapiens EST sequence. This sequence was generated as part of
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool YT lib. yEPD cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Teams/Feam69/.
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
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AL844307.1 GI:22019089
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mRNA linear EST 30-JUL-2002 sapiens cDNA, mRNA sequence.
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Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
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100.0%; Pred. No. 1.4e-140;
tive 0; Mismatches 0;
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/mol type="mRNA"
/mol type="mRNA"
/map="zef="taxon:9606"
/map="20"
/clone_lib="pool_YT_lib_v_SPD"
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                                                                                                                                                                                                                                                                                                                                                 Email: humquery@sanger.ac.uk
Sanger Centre name: sccd10816.154136A
Homo sapients EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool AK_lib v SPD cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Teams/Teams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams/Feams
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                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammallai Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Ashoroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 794)
                                                                                                                                                                                                           Homo sapiens BST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 2.2e-128;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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                          Homo sapiens (human)
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Matches 276; Conserv
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Contact: Robert Straubuels,
Email: cgapbs r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The J.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIO601 row: d column: 05
High quality sequence stops: 790.
High quality sequence stops: 790.
Totalon/Qualifiers
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11. (bases 1 to 960)
11. MGC tttp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 10545003 NIH_MGC_107 Homo sapiens cDNA clone
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100.0%; Pred. No. 1.1e-117;
ative 0; Mismatches 0;
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Tissue Procurement: ATCC
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Homo sapiens (human)
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Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name: sccdloM17.154136A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA ilbrary
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_FLU_lib_v_SPC cDNA library. Further information can be found
                                                                                                                                                                                                                                                                                                                                                      /dlone=IMAGE:673350"
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1 (bases 1 to 606)
Ashoroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln/B.G.E. Consortium/LLNL at: Plate: LLCM3049 row: m column: 21
High quality sequence stop: 628.
I. 960
Cocation/Qualifiers
I. 960
// Organism="MRNA"
// Ab_xref="MRNA"
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100.0%; Pred. No. 2.8e-92;
live 0; Mismatches 0; Indels (
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Substitution.

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Unpublished (2002)

Contact: The Sanger Centre

The Sanger Centre

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK

Email: hunquerySeanger. ac. uk

Sanger Centre name: sccdio816.400489A

Homo sapiens EST sequence. This sequence was generated as part of

The Wellcome Trust Sanger Institute program to identify and

annotate genes in the human qenome. Incomplete or unconfirmed genes

are experimentally analysed using a variety of cDNA library

resources. This sequence was obtained from a PCK product generated

from a pool of up to 100,000 cDNA clones derived from

pool AK lib v SPD cDNA library. Further information can be found at

http://www.sanger.ac.uk/Teams/Teams/Team69/.
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Ashoroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         968 TGTGTCCTGCAGAGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGTG
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at http://www.ganger.ac.uk/Teams/Team69/.
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Best Local Similarity 99.6%; Pred. No. 8.2e-90; Matches 250; Conservative 0; Mismatches 1
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/clone_lib="pool_AK_lib_v_SPD"
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/db_xref="taxon:9606"
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        Query Match
        9.8%; Score 116; DB 9; Length 642;

        Best Local Similarity 100.0%; Pred. No. 3.7e-47;
        3.7e-47;

        Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        Qy 1068 TCCTGTTTTCTGAAGCTGCCACAGGGAGGTCTTTTCAGGGGTCTCCGGGAGT 1127

        Db 588 TCCTGTTTTTCTGAAGCTGCAGGGAGGAGTCTTTTCAGTGAGGGTCTCCCGGAGT 529

        Qy 1128 CCCTCAGCTTCTACACTGGAGGAGGAGGAGGGTGTTTTGGATGATGCTAG 1183

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        Db 528 CCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTTTTTGGATGATGCTAG 473
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Search completed: February 20, 2004, 08:13:51 Job time : 2937 secs

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4;
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Patent No. 5776696
GENERAL INFORMATION:
APPLICANT: SALOWE, SCOTT P.
TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins
                        US-09-671-325-1598

US-09-220-3212-10

US-09-621-976-1574

US-09-328-352-1086

US-09-016-434-1255

US-09-016-434-1255

US-09-621-976-87

US-09-489-0394-5493

US-09-434-354-1

US-09-434-354-1

US-09-634-238-89

US-08-154-1

US-08-154-1

US-08-154-1

US-08-154-1

US-08-154-1

US-08-246-361A-37
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CITY: Rahway
STATE: NSA
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Lab Compatible
COMPUTER: Lab Compatible
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COMPUTER: PastSEQ for Windows Version 2.0
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PCT-US93-09945-1
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                                                                                                                                                                                                                                                                                                                               Sequence 10381, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Pro-
FILE REFERENCE: GENSET.054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
CURRENT FILING DATE: 2000-07-21
SOFTWARE: PATENT UPM
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US-09-621-976-10381
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Best Local Similarity
Matches 20; Conserv
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LENGTH: 539
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US-08-707-793A-3
TYPE: DNA
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Sequence 3, Appli
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Sequence 2, Appli
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-707-793A-3
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US-09-016-434-1452
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-09-099-053-1
-09-016-434-1101
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-09-276-531-78
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                                                                OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 1452, Application US/09016434

Sequence 1452, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: Word Perfect 6.1 for wind
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION BATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-(FELECOWUNICATION INFORMATION:
TELEPHONE: (650) 865-0555
INFORMATION FOR SEQ ID NO: 1452:
SEQUENCE CHARACTERISTICS:
    sTRANDEDNESS: single;
TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2129 base pairs
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Best Local Similarity 100.0
Matches 20, Conservative
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EDNESS: single
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CLONE: 9775207
US-09-016-434-1452
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US-09-016-434-1452
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nlarity 100.0%; Pred. No. 4;
Conservative 0; Mismatches 0; Indels
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APPLICANT: MARCY, ALICE
APPLICANT: SALOWE, SCOTT P.
APPLICANT: WISNIEWSKT, DOUGLAS
TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
TITLE OF INVENTION: PUSION PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTRY: NO
COMPUTRY: USA
ZIP: 07065-0900
COMPUTRY: READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,792A
FILING DATE: U4-SEP-1996
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
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                                 APPLICATION NUMBER: US/08/707,793A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CAMAZA: VALETA J
REGISTRATION NUMBER: 35,090
REFERENCE/DOCKET NUMBER: 19494
TELECHONICATION INFORMATION:
TELECHORE: 908-594-3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747 CCIICCICAICCGGGAGAGC 766
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; Sequence 3, Application US/08707792A
; Patent No. 5783398
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REGISTRATION NUMBER: 35,090
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 675 base pairs TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 04-SEP-19
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Matches 20; Conserv
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PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
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                              Sequence 3, Application US/09751389;
Patent No. 6630334;
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLARED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UNMER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASLSEQ for Windows Version 4.0
SOFTWARE: PASLSEQ for Windows Version 4.0
TYPE: DNA
CURRANT HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09579182

Sequence 2, Application US/09579182

Sequence 2, Application US/09579182

Patent No. 6506628

GENERAL INFORMATION:

APPLICANT: Robison, Keith B.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR FILE REFERENCE: MNI-161

CURRENT APPLICANTION NUMBER: US/09/579,182

CURRENT FILING DAID: 2000-05-25

NUMBER OF SEQ ID NOS: 7

SOFTWARE PATENTION OF SECOND OS: 7

SOFTWARE PATENTION OF SECOND OS: 7

SOFTWARE PATENTION OF SECOND OS: 7

SEQ ID NO 2

LENGTH: 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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1.7%; Score 20; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 19; DB 4; Length 1467;
100.0%; Pred. No. 12;
tive 0; Mismatches 0; Indels
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APPLICANT: Susan Onrust
APPLICANT: David Markby
APPLICANT: David Markby
APPLICANT: Sara Courtneidge
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: SAD RELATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412751 TGAGCAGGGAGAAAGCAGAG 412770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 TGAGCAGGGAGAAAGCAGAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(786431)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 AGGGCCTTCCTCATCCGG 760
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Patent No. 6388063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-579-182-2
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Gaps
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Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 POTTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATIVE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Scc...
100.0%; Pred. No. ...
                                   CITY: Los Angeles
STREET: SULLE *. California
COUNTRY: U.S.A.
ZIP: 90071-206

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORGE
COMPUTER: EMORGATIBLE
COMPUTER: EMORGATIBLE
COMPUTER: EMORGATIBLE
COMPUTER: TEME COMPATA;
MEDICATION NUMBER: US/09/099,053
FILING DATE: Herewith
CLASSIFICATION:
PRICK APPLICATION DATA;
APPLICATION NUMBER: 60/049,914
FILING DATE: Unne 18, 1997
ATTORNEY APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REPRERENCE/DOCKET NUMBER: 235/121
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: GASTON ON: 1:
SEQUENCE CHRARACTERISTICS:
SEQUENCE CHRARACTERISTICS:
LENGTH: 1548 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: MALL CURRENT APPLICATION DATA: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 AGGGGCCTTCCTCATCCGG 760
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-016-434-1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: PAI
STATE: CP
COUNTRY:
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Yes, Henry
APPLICANT: Yes, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION POR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS TWA
STREET: 3174 POPPUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Johnson, William G.
APPLICANT: Johnson, William G.
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REPERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                              Length 1438;
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                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 18; DB 4;
100.0%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.5%; Score 18; DB 3;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches
TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS FILE REFERENCE: PF-0631 US CURRENT APPLICATION NUMBER: US/09/470,946 CURRENT FILING DATE: 1999-12-22 EARLIER APPLICATION NUMBER: US 09/187,331 EARLIER FILING DATE: 1998-11-06 NUMBER: DESO ID NOS: 6 SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-318-448-8
; Sequence 8, Application US/09318448
; Patent No. 6210950
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1139 TACATCAGCCTGAATGAC 1156
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                                                                                                                                                                                                                                                                        ; FEATURE: -
; OTHER INFORMATION: 2705267
US-09-470-946-4
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-318-448-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-276-531-78/c
                                                                                                                                                                                SEQ ID NO 4
LENGTH: 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Guegler, Neil C.
APPLICANT: Guegler, Neil C.
APPLICANT: Guegler, Narl J.
APPLICANT: Guegler, Mariah R.
APPLICANT: Baughn, Mariah R.
ITILE OF INVENTION: CELL SURFACE GLYCOPROTEINS
FILE REFERENCE: PF-0611 US
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGRAM
SEQ ID NO 4
LENGTH: 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
1.6%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches
                                                           ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1305 Crdaggardgadacrdgrg 1323
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US-09-470-946-4
; Sequence 4, Application US/09470946
; Patent No. 6358923
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1139 TACATCAGCCTGAATGAC 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09187331
Patent No. 6043056
                                                                                                                                                                                                                                                                      2771 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: -
OTHER INFORMATION: 2705267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Corley, Neil C. APPLICANT: Guegler, Karl J APPLICANT: Gorgone, Gina A APPLICANT: Baughn, Mariah
                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 18; Conserve
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                      GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                      ; CLONE: 91256002
US-09-016-434-1101
                                                    CATION:
                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-187-331-4
                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                          STATE: WAA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
                           Sequence 1, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Bisppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
CORRESSPONDENCE ADDRESS:
ADDRESSES: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                      ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08822897C Patent No. 6380158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REFERSING/DOCKET NUMBER: 97-43
REFERENCE/DOCKET NUMBER: 97-43
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.4%; Scc
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 GTCCAGCCAGAGCATGC 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1...351
OTHER INFORMATION:
NAME/KEY: sig_peptide
LOCATION: 1...69
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 70...351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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COTHER INFORMATION:
US-09-046-479-1
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Patent No. 6410325

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Fraier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ARTHERSEION
FILE REPERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT PILING DATE: 2001-05-08
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
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1.5%; Score 18; DB 4; Length 70000;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 3; Length 3090;
Pred. No. 38;
                        COUNTEXT: USDA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
FILIND DATE: Herewith
CLASSIFICATION: NUMBER: USO/079,677
FILING DATE: March 27, 1998
CLASSIFICATION: MARCh 27, 1998
CLASSIFICATION: WINDER: 42,918
RETERRENCE/DOCKET NUMBER: PA-0008 US
REGISTRATION INFORMATION:
NAME: Lyon E. Murry, Ph.D.
REGISTRATION NUMBER: PA-0008 US
TELEFAX: (650) 855-055
TELEFAX: (650) 855-055
TELEFAX: (650) 855-055
TELEFAX: 3090 base pairs
TYPE: NUCLEIC acid
TOPOLOGY: Linear
INMEDIATE SOURCE:
TENDARY REALINGER:
TENDARY REALINGER:
TENDARY HRAINOTH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.5%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 38; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60708 GICCAAGGCCAGGGACCI 60725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 GGAGGAGTCTCTTCTCAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
CALIFORNIA
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: BRAINC
; CLONE: 1595762
US-09-276-531-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
US-09-851-896~3
```

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CORRESPONDENCE ADDRESS:
ADDRESSE: ZymcGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COLVEY: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATIOM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATIOM SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
SOFTWARE: FastSEG for Windows Version 2.0
SOFTWARE: EastSEG for Windows Version 2.0
SOFTWARE: FastSEG for Windows Version 2.0
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/822,897C
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SAWISLAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 37,438
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COCATION: 1..351
OTHER INFORMATION:
NAME/KEY: Sig_peptide
LOCATION: 1..69
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: 70..351
OTHER INFORMATION:
US-08-822-897C-1
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ö Query Match
1.4%; Score 17; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels δ

296 GTCCAGCCAGAGCATGC 312

57 Grccagccagacardc 41

Search completed: February 20, 2004, 08:16:02 Job time: 121 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

February 20, 2004, 07:26:02; Search time 486 Seconds (without alignments) 8523.550 Million cell updates/sec

Run on:

US-09-939-853A-74

1183 Title: Perfect score:

1 agctagagctccaaggaccc......tctctttggatgatgcctag 1183 Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

2308684 seqs, 1750822206 residues Searched:

4617368 Total number of hits satisfying chosen parameters: Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	ID	US-10-043-649-1	US-09-814-353-21302	US-09-867-550-953	US-09-867-550-95	US-09-867-550-19	US-09-864-761-28	US-09-864-761-15513	US-09-864-761-19612	US-09-814-353-17314	US-09-814-353-4631	US-09-814-353-10930	US-10-062-674-2188	US-10-027-632-195852	US-10-027-632-107077	
	DB	14	10	6	6	6	σ	0	6	10	10	10	15	15	15	
	Query Match Length DB	786	864	763	444	875	432	448	96	320	152	152	701	611	672	
ю	Query Match	62.1	61.2	55.5	29.4	28.8	11.3	11.3	8.1	7.4	6.5	6.5	1.8	1.7	1.7	
	Score	735	724	657	348	341	134	134	96	87	77	77	21	20	20	
	Result No.	Н	71	М	4	S	φ	7	œ	on	10	11	c 15	c 13	14	

				27,	954	1452		451	ന	Sequence 237, App	Sequence 13565, A	Sequence 20, Appl	Sequence 118578,	Sequence 55347, A	Sequence 11, Appl	25,	1, A	577, A	Sequence 1101, Ap	46381,	2048	261		1815		Sequence 26739, A	Sequence 38019, A	Sequence 270409,
0-027-632-14 0-027-632-14	0-027-632-26	260-238-64	-10-	3-2	-304-	US-10-305-720-1452	'n	US-09-908-975-4510	US-09-864-761-30106	0-072-60	864-761-3	US-09-789-561-20	-027	55	154-35	176-782-2	US-09-861-846-1	US-10-094-749-577	US-10-305-720-1101	US-10-369-493-46381	US-10-062-674-2048	US-09-738-626-3261	US-09-918-995-8609	US-09-983-965-1815	-027-632-	5-2673	US-09-918-995-38019	2-2704
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672 672	711	934	2017	2032	2129	2129	786431	65	114	510	599	1033	1125	1133	1467	1580	1833	2120	2771	4207	4720	204	402	403	474	487	491	497
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16	18	19	20	21	22	23	24	25	c 26	27	71	c 59	m	31	32	33	34	35	36	m	c 38	39	40	41	42	43	44	4. ญ

ALIGNMENTS

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wu, Jun

APPLICANT: Zhou, Xiulan

APPLICANT: Shen, Mary

APPLICANT: Shen, Mary

APPLICANT: Shen, Mary

APPLICANT: Shen, Mary

APPLICANT: Shen, Mary

TITLE OF INVENTION: Cloning of a No. US20030059924Alel Inhibitor of Antigen-receptor for INVENTION: Cloning of a No. US20030059924Alel Inhibitor of Antigen-receptor for INVENTION: Retroviral-based Functional Screen

TITLE OF INVENTION: Retroviral-based Functional Screen

TITLE OF INVENTION: Retroviral-based Functional Screen

TITLE OF INVENTION: Retroviral-based Functional Screen

CURRENT FILING DATE: 2002-01-10

NUMBER OF SEQ ID NOS: 3

SOFTWARE PATENTION OF STATE OF SEQ ID NOS: 3

SOFTWARE PATENTION OF STATE OF SEQ ID NOS: 3

SOFTWARE PATENTION OF STATE OF SEQ ID NOS: 3

SEQ ID NOS: 3

LENGTH: 786

TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE:
                                                Sequence 1, Application US/10043649
Publication No. US20030059924A1
                                                                                                                                                                                                               APPLICANT: Holland, Sacha J.
APPLICANT: Mendenhall, Marcy K.
APPLICANT: Spardo, Jorge
APPLICANT: Spencer, Collin
APPLICANT: Fu, C. Alan
APPLICANT: Luo, Ying
APPLICANT: Payan, Donald G.
APPLICANT: Mancebo, Helena S.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(786)
; OTHER INFORMATION:
US-10-043-649-1
US-10-043-649-1
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62.1%; Score 735; DB 14; Length 786;

Query Match

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54 GCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGCCCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 CCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 TCGATGATGATTCTGAGTGCTCTGCTGAGGAACAATGGGGAAGTCTGCCCAGCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 GCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGACGGTGCTGTCTGAAGTCTCAGGCAGAGTATAACATCCCCAGCGTCCACGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 CTTCCCTCCTGGCTGGCTGTGCTTGGGAGGTTCCCCAGTCCAGAATCCCTAAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 CCTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCAAAGCCCTAACCTGTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 AAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTCCAAGGCCAGGGACCTGTGACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTAGAGCTCCAAGGACCCCACGCCTGTGTCTCTGTGACAGAGCTCAAAGGGCCCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0;
0; Mismatches 1;
CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 60/211,940

PRIOR APPLICATION NUMBER: US 60/216,820

PRIOR APPLICATION NUMBER: US 60/216,820

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

NUMBER OF SEQ ID NOS: 22037

SOFTHARE: PASESEQ for Windows Version 4.0

LENGTH: 864
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113 121 173 181 233 241 293 301 353 361 413 421 473 481 533 541 593 601 653 661 713

61

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| Sequence 951, Application US/09867550
| Patent No. US2002003206A1
| GENERAL INFORMATION:
| APPLICANT: Leach, Martin D.
| APPLICANT: Conley, Pamela
| APPLICANT: Conley, Pamela
| APPLICANT: Topper, James
| APPLICANT: Topper, James
| TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and I:
| TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and I:
| TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and I:
| TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and I:
| TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and I:
| TITLE OF INVENTION NUMBER: US201-09-20
| PRIOR FILING DATE: 2001-09-20
| PRIOR FILING DATE: 2001-09-20
| SOFTWARE: FastSEQ for Windows Version 4.0
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 951
| LENOTH: 444
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                                                         TGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGAGAAGCAGAGGAAC
                                                                                                                                                                                                                                                       665 GAGGCTCTTACTCTGTCAGTCGCCCTCAGCCGCCTGCATCTGGGACCGGATCAGAC
                                                                                                                                                                       recretricritaccressasceresasceresecrirecrearecessascesea
                                                                                                                                                                                                                    777 GAGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCCTGCATCCTGGGACCGGATCAGAC
                                                                                                                            TGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATCCGGGAGAGCCAGACCAGGA
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29.4%; Score 348; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 7.5e-167;
Matches 348; Conservative 0; Mismatches 0;
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US-09-867-550-951
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Panela
APPLICANT: Conley, Panela
APPLICANT: TOPPET, James
APPLICANT: TOPPET, James
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: NUMBER: US(90/867,550
CURRENT APPLICATION NUMBER: US(90/867,550
PRIOR PILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US(0/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SSOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 953
LENGTH: 763
    721
                                                 773
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                             AAAGTCTCCCATGGGTGGCTGTATGAGGCCCTGAGCAGGAAAAGCAGAAAGTGCTG
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Pred. No. 0;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                  Sequence 953, Application US/09867550 Patent No. US20020082206A1
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Best Local Similarity 99.7%;
Matches 757; Conservative C
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ORGANISM: Homo sapiens
US-09-867-550-953
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989 CCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGG 1048
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100.0%; Pred. No. 8.3e-58;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-26
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 92/632,366
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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Best Local Similarity 100.
Matches 134; Conservative
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CRGANISM: Homo sapiens
CRGANISM: Homo sapiens
CATHER INFORMATION: EXPRE
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US-09-864-761-15513
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US-09-864-761-2829
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                                                                                                                                     APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21407-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09-20
PRIOR FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1915
LENGTH: 875
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Betent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PILING DATE: 2000-02-04
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Best Local Similarity 100.0%; Pred. No. 2.5e-163;
Matches 341; Conservative 0; Mismatches 0;
                                           915, Application US/09867550
US20020082206Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION DATE: 2001-05-23
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N HELA, SIGNAL = 1.9
N HELA, SIGNAL = 1.9
N HELAO, SIGNAL = 2.1
N HEART, SIGNAL = 2.1
N HEART, SIGNAL = 2.3
N FEFFAL LIVER, SIGNAL = 2.3
N LUNG, SIGNAL = 1.7
N BONE MARROW, SIGNAL = 2.3
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PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-3
PRIOR PILING DATE: 2000-03
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PRIOR PILING DATE: 2000-03
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PRIOR PILING DATE: 2000-09-37
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PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                               Sequence 19612, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRESSED IN EXPRE
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ORGANISM: Homo sapiens
FEATURE:
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                                                           PRESENT NO. USESURIONGENERAL INFORMATION:
APPLICANT: Perm, Sharron G.
APPLICANT: Perm, Sharron G.
APPLICANT: Sank, David R.
THILL GANT: CHANGEN WESTERN G.
APPLICANT: Sank, David R.
THILL GANT: CHANGEN WESTERN G.
THILL GANT: CHANGEN G. CAN CHANGE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR THILL GANTE CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. CAN CHANGEN G. C
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CHER INFORMATION: MAP TO AL031662.24
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
US-09-864-761-15513
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11.3%; Score 134; DB 9;
Best Local Similarity 100.0%; Pred. No. 8.2e-58;
Matches 134; Conservative 0; Mismatches 0;
Sequence 15513, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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FEATURE:

NAME/KEY: misc feature

LOCATION: 17, Î02, 112

OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4631
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                                                                                                                967 CTGTGTCCTGCAGAGGGCTGGCCCGCTCCCTGGCAAGGATATACCCCTACCTGTGACTGT 1026
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
IITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                  ;
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; OTHER INFORMATION: EST_HUMAN HIT: AI125308.1, EVALUE 2.10e-01
US-09-864-761-19612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
                                             Query Match
8.1%; Score 96; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                               1027 GCAGAGGACACCACTCAACTGGAAAGAGCTGGACAG 1062
                                                                                                                                                                                                              61 GCAGAGGACACCACTCAACTGGAAAGAGCTGGACAG 96
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100.0%; Pred. No. 7.6e-34;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 87; Conservative
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US-09-814-353-17314
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US-09-814-353-4631
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549 TGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGGACTGGTGGACGG 608
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US-09-814-333-10930

| Sequence 10930, Application US/09814353
| Publication No. US20030165831A1
| GENERAL INFORMATION:
| APPLICANT: Lee, John
| APPLICANT: Lillie, James
| TITLE OF INVENTION: NOTEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: NOTEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: NOTEL GENES, COMPOSITION, AND
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Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 77; Conservative 0; Mismatches 0;
FILE REFERENCE: MRI-066B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/09/814,353
FRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSECSE FOR WINDOWS VETSION 4.0
SEQ ID NO 4651
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| JERNERAL INCHARATION:
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| JENERAL INCHARATION: POLYMOLPHISMS in the Human Genome | TITLE OF INVENTION: POLYMOLPHISMS in the Human Genome | TITLE OF INVENTION: POLYMOLPHISMS in the Human Genome | FILE REPERENCE: 108827.129 | CURRENT PELING DATE: 2002-04-30 | PRIOR PELING DATE: 2000-07-12 | PRIOR PELING DATE: 2000-07-12 | PRIOR PELING DATE: 2000-07-12 | PRIOR PELING DATE: 2000-03-29 | PRIOR PELING DATE: 2000-03-29 | PRIOR PELING DATE: 2000-03-29 | PRIOR PELING DATE: 2000-03-29 | PRIOR PELING DATE: 2000-03-29 | PRIOR PELING DATE: 1999-11-23 | PRIOR PELING DATE: 1999-11-23 | PRIOR PELING DATE: 1999-11-23 | PRIOR PELING DATE: 1999-11-23 | PRIOR PELING DATE: 1999-09-28 | PRIOR PELING DATE: 1999-09-28 | PRIOR PELING DATE: 1999-09-28 | PRIOR PELING DATE: 1999-08-09 | NOWBER FEASESO-FOR PRIOR PELING DATE: 1999-08-09 | SOFTWARE FEASESO-FOR PRIOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09 | SOFTWARE FEASESO-FOR PELING DATE: 1990-08-09
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Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 611; 9.6;
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100.0%; Pred. No. 9.5;
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    PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FBALESEQ for Windows Version 4.0
SEQ ID NO 195852
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Conservative 0; Mismatches
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
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; ORGANISM: Human
US-10-027-632-195852
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US-10-027-632-107077
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US-10-027-632-142058
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US-10-027-632-107077
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Publication No. US20040005559A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LORING, Jeanne F.; Kaser, Matthew R.
TITLE OF INVENTION:
MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFERENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SSCHWARE: PERL PROGRAM
SEQ ID NO 2188
LENGTH: 701
                                                                                                                                                                                                                                                                                                                                                                                                        25 TGTCGCTGAGACTCGGGGAGCCATTGACCATCGTCTCTGAGGATGGAGCTGGTGGAGGACGG
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// Sequence 195852, Application US/10027632

// Sequence 195852, Application US/10027632

// Sequence 195852, Application US/10027632

// Sequence 195852, Application US/0027632

// SPECIAL INFORMATION: Identification and Mapping of Single Nucleotide

// TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

// TITLE OF INVENTION: Polymorphisms in the Human Genome

// TITLE OF INVENTION: Polymorphisms in the Human Genome

// TITLE OF INVENTION: POLYMORER: US/10/027,632

// CURRENT APPLICATION NUMBER: US 60/198,676

// PRIOR PAPLICATION NUMBER: US 60/198,676

// PRIOR APPLICATION NUMBER: US 60/193,483

// PRIOR PILING DATE: 2000-04-20

// PRIOR PILING DATE: 2000-03-29

// PRIOR PILING DATE: 2000-03-29

// PRIOR PILING DATE: US 60/193,483

// PRIOR PILING DATE: US 60/195,218
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0
                                                                                                                                                                                            Length 152;
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1.8%; Score 21; DB 15; Length 701;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 893157.1
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6.5%; Score 77; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 77; Conservative 0; Mismatches 0;
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| NAME/KEY: unsure
| LOCATION: (1) ... (701)
| OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-2188
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; NAME/KEY: misc_feature; LOCATION: 17, 102, 112; CTHER INFORMATION: n = A,T,C or GUS-09-814-353-10930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 TGCTGTCTGAAGTCTCA 625
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ORGANISM: Homo sapiens
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Query Match
1.7%; Score 20; DB 15; Length 672;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: Polymorphisms in the Human Genome
[FILE REPERENCE: 108827.129
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[CURRENT ELING DATE: 2002-04-30
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Run on:

February 20, 2004, 08:14:02; Search time 93 Seconds (without alignments) 792.956 Million cell updates/sec

Title: Perfect score:

US-09-939-853A-75 1353 1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA 261 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Aau91308 Human pro	_	187 Human	357 Human	2993	5456 Mouse	Mouse	Human	Human		Human	03 Src-li	8696	2 Novel	Human	4 Human	Human	Human	Aay49420 PKA subst	Abr58699 Human can	Human	0	72 Tumour	00 Human 1	2 Human
		ΔI	913	AA015457	ABP52187	AAE26357	AAB42993	AA015456	AA015458	ABP64788	ABP64107	ABP64588	ABP52188	ABU79103	σ	AAU31072		ADD19014	AAB99332	ABW01407	AAY49420		ADE40449	ABR59690	ABG79672	AAB37700	ADE58802
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dю	Query	Match		φ.	σ,	ο,	ω,	ů,	69.1	œ	•	ω.	35.6	•	'n	34.8	ო	7.	26.6	œ W	'n	'n	Š	S	25.1	'n	25.1
		Score	1353	1347	1347		9	02	934.5	m.	N	586	ä	481.5	91.	70.	52.	ö	60.	60.	4	4	4	4	4	340	340
	Result	No.	1	8	m	4	ស	9	7	00	თ	10	11	12	13	14	15	16	17	60 €	19	20	21	22	23	24	25

Human Pro		Novel hum	Tumour in			Human Pro							Xenopus 1	Xenopus 1	Human yes	Human 145	Novel	Human	Mutant
Ade58799	Abr56202	Abq05994	Abq79673	Abbs7957	Aau74614	Add45918	Add14129	Aab84663	Abq10302	Ada00843	Aav29668	Aau08734	Aau08730	Aau08735	Aay24421	Ade31767	Abq22264	AdC99048	Aav44449
ADE58799	ABR56202	ABG05994	ABG79673	ABB57957	AAU74614	ADD45918	ADD14129	AAB84663	G10302	A00843	AAY29668	AAU08734	AAU08730	PAU08735	AAY24421	ADE31767	ABG22264	ADC99048	AAY44449
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7	7	0	7	7	. 2	2	7	3	24	9	2	4,	4.	4	2	7	4		ω
20	509	7	26	21,	54	53	53	5.4	54.	54.	49	496	496	496	54.	525	55.	458	53.
25.1	25.1	25.0	24.9	24.5	23.4	23.3	23.3	23.3	23.3	23.3	23.2	23.2	23.2	23.2	23.2	23.1	22.7	22.4	21.2
340	4	338	ന	332	317	315.5	315.5	315.5	315.5	315.5	313.5	313.5	313.5	313.5	313.5	312.5	306.5	303	286.5
56	27	58	59	30	31	32	33	34	S)	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis; call signal processing disorder; metabolic pathway modulation disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; adequired immunodeficiency syndrome; AIDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy. AAU91308 standard; protein; 261 AA. (first entry) Human protein NOV13. 18-JUN-2002 AAU91308;

Homo sapiens.

WO200216599-A2.

28-FEB-2002.

27-AUG-2001; 2001WO-US026510.

; 2000US-0228191P. ; 2001US-0267300P. ; 2001US-0269961P. ; 2001US-0277337P. 08-FEB-2001; 20-FEB-2001; 20-MAR-2001; 25-AUG-2000;

(CURA-)

CURAGEN CORP.
COR THERAPEUTICS INC. (CORT-)

Shimkets RA; Grosse WM, Hart M, Kekuda R, Shi Tomlinson JE, Topper JN, Yang R; Conley PB, Szekeres ES, Burgess CE, Spytek KA,

WPI; 2002-280937/32. N-PSDB; ABK61465.

New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.

Claim 3; Page 98; 263pp; English.

The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%), the nucleotide encoding NOVX (or its complement, fragment or variant). NOVX is NOVI-14,

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and antibody against it, are useful for treating or preventing (e.g. by an antibody against it, are useful for treating or preventing (e.g. by atheroscierosis, a Novx-associated disorder in humans, e.g. cardiomyopathy, atheroscierosis, a Misorder felaced to call signal processing and metabolic pathway modulation, diabetes or cancers. The Novx polypeptide metabolic pathway modulation, diabetes or cancers. The Novx polypeptide predisposition to the disease. The Novx nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancers), immune response, graft-versus-host disease, acquired cancer), immune response, graft-versus-host disease, hypertension, congenital heart defects, multiple sclerosis, inflammation or Albright herating the conditions. This is also useful in detection assays, creating the conditions. This is also useful in detection assays, chromosome mapping, issue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a NOVX protein
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Sequence 261 AA;

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                                                                                                                                                    61 IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
                                                                                                                                                                                           61 IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
                                                                                                                                                                                                                                  121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180
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                                                                             1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT
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                                        Gaps
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0
  Length 261;
                                        Indels
100.0%; Score 1353; DB 5; 100.0%; Pred. No. 1.6e-130;
                                      0; Mismatches
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                  Best Local Similarity 100.
Matches 261; Conservative
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                                                                                                                                                                                                                                                                                                           181
  Query Match
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AAO15457 standard; protein; 261 AA (first entry) 03-OCT-2002 AA015457; RESULT 2

Human; gene therapy; modulator of antigen receptor signalling; MARS; tumour suppressor gene; Sor-like adaptor protein; SiAP; myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer. Human modulator of antigen receptor signalling (MARS) protein.

Homo sapiens

30-MAY-2002

WO200242452-A2

26-NOV-2001; 2001WO-CA001662

27-NOV-2000; 2000CA-02324663

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The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Scr-like adaptor protein (SLAP): The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present amino acid sequence represents a human MARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEBSLLSEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                             New isolated modulator of antigen receptor signaling protein or its. fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
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99.6%; Pred. No. 6.8e-130;
tive 0; Mismatches 1;
(HOSP-) HOSPITAL FOR SICK CHILDREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRESLSFYISLNDEAVSLDDA 261
                                                                                                                                                                                                           Claim 7; Fig 9A; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                        N-PSDB; AAL44089
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 261 AA;
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120 120 180 180 240

9 9

> Human Src-like inhibitory molecule (SLIM) protein. 15-OCT-2002 (first entry)

LRESLSFYISLNDEAVSLDDA 261

241

RESULT 3 ABP52187

ABP52187 standard; protein; 261

ABP52187;

Human, Src-like inhibitory molecule, SLIM, Src-like adapter protein, SLAP, inhibitor; antiinflammatory; immunosuppressive; anti-HIV; andulator; lymphocyte; CD1; gene therapy; immunodeficiency disorder; acquired immune deficiency syndrome; AIDS; acute-inflammatory disorder; chronic inflammatory disorder; autoimmune disorder; transplant rejection.

Homo sapiens

WO200255707-A2

18-JUL-2002

us-09-939-853a-75.rag

AAE26357;

Luo Y; Sheng N;

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The present sequence represents the human Src-like inhibitory molecule (SilM) protein (I). The present invention describes a SLIM protein comprising an N-terminal myristylation sequence, an N-terminal SH2 domain, and an N-terminal myristylation sequence, an N-terminal SH2 domain which can N-terminal SH2 domain which is unable to bind to CDI. (I) has antiinflammatory, immunosuppressive and anti-HIV activities, and can be used as a modulator of lymphocyte activation, and of ubiquitination of a CDI target protein and in gene therapy. (I) is useful for screening a bioactive agent capable of binding to SLIM. (I) is also useful for screening a bioactive agent capable of the streatment of conditions which involves this function or dysregulation of SLIM protein activity, is useful in the study or in the treatment of conditions which involves this function or dysregulation of SLIM protein activity, is to diagnose, treat or dysregulation of SLIM protein activity, is to diagnose, treat or prevent SLIM associated disorders. (I) or the polynuclectide encoding it (II) is useful for modulating and activation in lymphocytes and/or platelet activation, for modulating and activation in lymphocytes and/or planelocytes. (I) or is also useful in the treatment of immunodeficiency disorders, such as acquired immunodeficiency syndrome (AIDS), for the prevention and treatment of acute inflammatory disorders, chronic inflammatory activation and transplant rejection
                                                                                                                                                                                                                                                              New src-like inhibitory molecule protein, useful for treating immunodeficiency disorders and inflammatory disorders, comprises N-terminal myristylation sequence, SH2 domain and/or SH3 domain.
                                                                                                                                    C, Fu AC,
                                                                                                                                    Spencer C,
Shen M,
                                                                                                                                 Pardo J, ;
, Zhou X,
                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 2A; 91pp; English
                                                                                                                                                         Wu σ,
  10-JAN-2002; 2002WO-US000718
                                          10-JAN-2001; 2001US-0260953P
                                                                                                                                 Mendenhall MK,
                                                                                       (RIGE-) RIGEL PHARM INC
                                                                                                                                                       Mancebo HS,
                                                                                                                                                                                               WPI; 2002-575432/61.
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                                                                                                                                 SJ,
                                                                                                                                                       Payan DG,
                                                                                                                                 Holland
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ò 240 RESQTREGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180 DDICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKBLDSSLLFSEAATGEBSLLSEG 240 IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120 121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELA 180 1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60 9 MGSLPSRRKSLPSPSLSSSVQGQCPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT IVSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI DDICCLIKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEG Gaps ò Length 261; 1; Indels 99.6%; Score 1347; DB 5; 99.6%; Pred. No. 6.8e-130; iive 0; Mismatches 1; LRESLSFYISLNDEAVSLDDA 261 LRESLSFYISLNDEAVSLDDA 260; Conservative Local Similarity 61 61 241 Query Match 121 181 181 241 Matches ò g ð 엄 à 유 ò g 8

AAE26357 standard; protein; 261 AA

RESULT 4 AAE26357

ΩX

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Human; SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2; SLAP-2; immune disorder; signal transduction; autoimmune disease; cancer; neoplasm; inflammation disorder; rheumatoid arthritis; osteoarthritis; psoriasis; rhinitis; allergy; inflammatory bowel disease; gene therapy; cofn's disease; systemic lupus erythematorsus; tissus/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kanner SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Perez-Villar JJ,
                                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                   note= "Tyrosine phosphorylation site"
                                                                                                                                                                                                                                                                                              site"
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                                    Human Src-Like Adapter Protein-2 (hSLAP-2).
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                                                                                                                                                                  15...90
/note= "SH3 domain"
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                      94. .176
/note= "SH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2001; 2001WO-US043367.
                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2000; 2000US-0252545P.
                   (first entry)
                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD43980.
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                                                                                                                                    Homo sapiens
                 13-DEC-2002
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                                                                                                                                                       Key
Domain
                                                                                                                                                                                                       Domain
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Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic intervention in immunological and inflammatory disorders and cancer.

Claim 9; Fig 2; 85pp; English.

The invention relates to a substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-like Adapter Protein-2 (SLAP-2). The invention is useful for treating an immune disorder involving hyperactivity of B- or T-lymphocytes in a mammal. The invention is useful for screening for antagonists or inhibitors of the interaction of histap-2 with cellular signalling compounds, for disponsing, treating or preventing diseases or disorders associated with aberrant or uncontrolled collular signal transduction, for determining those cellular signalling molecules which associate with hSLAP-2 and which provide critical signals for cell activation, and as effectors in methods to affect T-cell activation. The invention is useful in screening assays to identity and detect candidate bloactive agents that modulare hSLAP-2 biocactivity, for potential use to treat autoimmune diseases which may be caused by hyperactivated B cells, as well as to treat diseases which may be caused by hyperactivated T cells, in addition to other immune system related conditions, diseases, or disorders, T-cell and B-cell neoplasms, inflammation disorders, diseases and conditions, rheumatoid arthritis, ostecarthritis, psoriasis, rhinitis, inflammatory bowel disease (Crohn's CURA-) CURAGEN CORP.

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240
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and ulcerative colitis), allergies, particularly those involving hyperactivity of B-cells and T- cells, or other immune cells, such as mast cells or ecainophils, autoimmune diseases such as systemic lupus erythematosus and multiple sclerosis, pulmonary diseases including asthma, acute respiratory distress syndrome, and chronic obstructive pulmonary disorder, tissue/ organ rejection and cancer. The invention is useful in gene therapy. The present sequence is human SLAP-2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1347; DB 5; Length 261; 99.6%; Pred. No. 6.8e-130; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2757 polypeptide sequence SEQ ID NO:5514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42993 standard; protein; 248 AA
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99US-0127728P.
2000US-00540763.
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 99.6
nes 260; Conservative
                                                                                                                                                                                                                                                                                 Sequence 261 AA;
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05-APR-1999;
30-MAR-2000;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX completes are extracted as: cytostatic; hepatotropic; vulnerary; antipartise such as: cytostatic; hepatotropic; vulnerary; antipartise; antipartise such as: cytostatic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; or cardiant; thrombolytic; coagulant; vasotropic; anticibatic; hypotensive; dermatological; antifungal; antirhymosit; antibacterial; antiviral; antifungal; antirheumatic; antithymoid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders osteoarthritis, graft vs host disease, cardiovascular disease, disorders mellitus, hypertension, hopethyroidism, cholesterol ester storage, systemic lupus erythematoaus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allargies, aplastic ansemia, burns, wounds, hone and cartilage damage, nocturnal haemoglobinuria, antiliflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 RLSRPASWDRIRHYRIHCLDNGWLYISPRLIFFSLQALVDHYSELADDICCLLKEPCVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 RAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGBESLLSEGLRESLSFYISLNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SLSSSVQQQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SLSSSVQGQGPVTMEAERSKATAAALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 RAGPLPGKDIPLPVTVQRTPLNWKBLDSSLLFSEAATGEESLLSEGLRESLSFYISLNDE
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                                                                                                                                                              Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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Best Local Similarity 98.8%; Pred. No. 6.8e-122;
Matches 244; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                            Claim 11; Page 4693-4694; 5507pp; English.
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                                                                                                                     N-PSDB; AAC77202
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                                                Shimkets RA,
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Mouse, gene therapy, modulator of antigen receptor tumour suppressor gene, Scr-like adaptor protein: S
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Matches 184; Conserv
                                                                                                                                                                                                                                                N-PSDB; AAL44090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 210 AA;
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                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumours suppressor gene and exhibits structural and sequence similarity to the Sor-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myelogenoliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present amino acid sequence represents a mouse MARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I.SEDGDWWTVQSEVSGREYHMPSVYVAKVAHGWLYEGLSREKAEELLLLEPGNPGGAFLI
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myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse modulator of antigen receptor signalling short isoform protein.
                                                                                                                                                                                                                                New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%; Score 1028; DB 5; 79.4%; Pred. No. 4.9e-97; ive 16; Mismatches 34;
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                                                                                                                                                                                                                                                                               Claim 7; Fig 1A; 110pp; English.
                                                                                                     26-NOV-2001; 2001WO-CA001662
                                                                                                                          27-NOV-2000; 2000CA-02324663
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Best Local Similarity 79.4'
Matches 208; Conservative
                                                                                                                                                                         Loreto MP;
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                                                       WO200242452-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RESOTREGSYSLSVELSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLOALVDHYSEGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present amino acid sequence represents a mouse MARS
                               tumour suppressor gene; Scr-like adaptor protein; SLAP; myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMRABRSKATAVALGSFPAGGPAELSLRLGEPLT
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signalling; MARS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 934.5; DB E Pred. No. 1.5e-87; 3; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LADDICCLLKEPCVLQRAGPLP 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOSP-) HOSPITAL FOR SICK CHILDREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP64788 standard; protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 78; 110pp; English.
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88.9#;
                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2001; 2001WO-CA001662.
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central nervous system disease; viral infection;
peripheral nervous system disease; non-healing wound; infectious disease;
immune deficiency; immune disorder; bacterial infection; allergy; cancer;
fungal infection; autoimmune disorder; coagulation disorder; nootropic;
antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
   expressed sequence tag; EST; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Zhou P, Asundi V, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 448; 394pp; English.
                                                                                                                                                                                                                                         immunostimulant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2001; 2001WO-US042950.
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ue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABQ99374
                                                                                                                                                                                                                                                                                                                                                                         WO200259260-A2
                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F,
NAME OF THE OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OW
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Zhang J, Zhao QA;

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The present invention relates to novel human coding sequences (ABO99268-ABO9608) and proteins (ABP64682-ABP65022). The sequences are useful in the research methods. The polynucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The colynucleotides are useful in diagnostics as expressed sequence tags (ESTS) for identifying expressed genes or for physical mapping of the numan agnome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoidetic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, allergic viral, bacterial or fungal infection, autodimmne disorders, allergic reactions and conditions, coagulation were assembled from ESTS collated mainly by sequence of the invention will be seminated from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 87.5
nes 182, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 210 AA;
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Matches
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                              121 RESOTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLOALGDHYSEGW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORPX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSE--
                                                                                                                                                                                                                                                                                                                                       Cytostatic; Cardiant, Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilincal vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy, autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.
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Best Local Similarity 99.4%; Pred. No. 1.5e-76;
Matches 158; Conservative 0; Mismatches 1; Indels
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                                                                     ----LADDICCLLKEPCVLQRAGPLP 200
                                                                                          181 PAPWQGYTPICDCAEDTIQLERAGQLP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 954; 78pp; English.
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                                                                                                                                                                                              ABP64107 standard; protein; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2001; 2001US-00867550.
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                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LEAC/) LEACH M D.
(MEHR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-626554/67.
N-PSDB; ABQ98670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                     04-NOV-2002
                                                                                                                                                                                                                                                                                                      Human ORF477
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121
                                                                     179
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                                                                                                                                                      RESULT 9
ABP64107
ID ABP6
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0; Gaps

Length 113; Indels

43.3%; Score 586; DB 5; L 100.0%; Pred. No. 4.7e-52; ive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 112, Conservative

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150 IHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLPGKDIPLPVT 209

2 IHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGPLPGKDIPLPVT 61

Human Src-like adapter protein (SLAP).

15-OCT-2002 (first entry)

ABP52188 standard; protein; 276 AA

ABP52188

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61 IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHCWLYEGLSREKAEELLLLPGNPGGAFLI 120
                                                                INSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
                         9
MGSLPSRRKSLPSPSLSSSVQGQGPVTMBABRSKATAVALGSFPAGGPAELSLRLGEPLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or
                    1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT
                                                                                                                                                                                                                                                                    Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Law D;
                                                                                         121 RESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLY 159
                                                                                                          Conley PB, Topper JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; SEQ ID NO 1916; 78pp; English.
                                                                                                                                                                            ABP64588 standard; protein; 113 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000US-0208427P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leach MD, Mehraban F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease.
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MEHRABAN F.
CONLEY P B.
TOPPER J N.
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                                                                                                                                                                                                                                               Human ORF958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAWD/)
                                                                                                                                                  RESULT 10
ABP64588
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The present invention describes the human Src-like inhibitory molecule (SLIM) protein (I). The present invention describes a SLIM protein (C comprising an N-terminal myristylation sequence, an N-terminal SH3 domain which can bind to Cb1, or comprising an N-terminal SH3 domain which can bind to Cb1, or comprising an N-terminal SH3 domain which can bind to Cb1, or comprising an N-terminal SH2 domain which co is unable to bind to Cb1. (I) has antifilfammancory, immunosuppressive and can the transport of lymphocyte activation, and of ubiquitination of a Cb1 target protein, and in gene cherapy. (I) is useful for screening a bioactive agent capable of binding Ct os SLIM. (I) is also useful for screening a bioactive agent capable of modulating SIIM binding. (I) or its fragments is useful in the study or cyprevent SIIM associated disorders. (I) or the polymorleotide encoding it (II) is useful for modulating alwocyte and/or platelet activation, for modulating and activation in modulating and activation in lenkocyte and/or platelets and for modulating and activation in lenkocyte and/or mast cells. (I) or is also useful for modulating the basal activity of lymphocytes. (I) is useful in the treatment of immunodeficiency disorders, such as
                                                                                                                                              Human, Src-like inhibitory molecule, SLIM, Src-like adapter protein, SLAP, inhibitor; antinflammatory, immunosuppressive; anti-HIV, modulator; lymphocyte, CDl, gene therapy; immunodeficiency disorder, acquired immune deficiency sydacome; AIDS, actte inflammatory disorder; chronic inflammatory disorder; autoimmune disorder; rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luo Y;
Sheng N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New src-like inhibitory molecule protein, useful for treating immunodeficiency disorders and inflammatory disorders, comprises terminal myristylation sequence, SH2 domain and/or SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spencer C, Fu AC,
Shen M, Liao XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pardo J, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 2B; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendenhall MK, Pa
                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2002; 2002WO-US000718.
                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2001; 2001US-0260953P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mancebo HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-575432/61.
                                                                                                                                                                                                                                                                                                           WO200255707-A2.
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SJ,
                                                                                                                                                                                                                                                                                                                                                18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Payan DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holland
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The present invention relates to novel human ORFX polypeptides and their coding sequences (ABPG5611-ABPG4681 and ABC98194-ABD99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HVVBC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood for this pater of form pater of the printed specification, but was sequated in electronic format directly from the USPTO web site at sequence.html?DocID=20020082206

Sequence 113 AA

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128
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                                                                                                                                                                                                                                                                                                                 119 FYSLSVR-----HRQVGHYRIFRLPNNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLT 172
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                                                                                                                                                                                                                                                                                                                                                                         173 TPCLTQSTAAPAVRASSSPVTLRQKTVDWRRVSR---LQEDPEGTENPLGVDESLFSYGL 229
                                                                                                                                                                                                                                                                                                SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          staphylococcal enterotoxin; tumour; cancer; apoptosis;
                                                                                                                                                                                      68
                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, by binding
ling induces anergy or apoptosis
acquired immunodeficiency syndrome (AIDS), for the prevention and treatment of acute inflammatory disorders, chronic inflammatory disorders, autofimmune disorder and transplant rejection. The present sequence represents the human Src-like adapter protein (SLAP), which is given in comparison with the human SLIM protein in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptos: gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
                                                                                                                                                                                                   WIVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRG
                                                                                                                                                                                                                                                                                                                                                         -----EESTISEGI
                                                                                                                                                                                   KSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDW
                                                                                                                                                          Gaps
                                                                                                                                                        Indels 23;
                                                                                                                               Length 276;
                                                                                                                                                                                                                                                                                                                                                      EPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG
                                                                                                                                                     85;
                                                                                                                             DB 5;
                                                                                                                            ; Score 481.5; DB 5; Pred. No. 1.1e-40; 43; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian cell receptor, useful in the trea
o tumor associated lipids where the binding
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in T cells and antigen presenting cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU79103 standard; protein; 276 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Src-like adpator protein, SLAP.
                                                                                                                             35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                             RESLSFYISLNDE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESIASYLSLTSE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                            Query Match
Best Local Similarity 40.3%
Matches 102; Conservative
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                                                        given in comparison
present invention
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                                                                                                  Sequence 276 AA;
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anergy or apoptosis in the T cells and antigen presenting cells (APCS). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (INI) a tumouricidal immunocyte population in vivo in a mammal control of allowing tumour associated lipids to context immunocytes in which receptors for immunosuppressive facty acids, ceramides, glycolipids, glycosphingolipids, glycolipids, glycolipids, glycolipids, glycolipids, glycolipids, libopeptides and proteoglycolipids, gangliosides, simplated glycoms, libopeptides and proteoglycolipids are inactivated or uncertaint to the treatment of cancer (where m adaptor protein which inhibite I cell activated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen) protein which cancer (comprising a lipid raft conjugated to a superantigen) protein which inhibit a curvated immunocyte population as vivo in a mammal (by a tumouricidal immunocyte population, and administering the tumouricidal lipids to context APCS, in which receptors for the tumour associated lipids to context APCS, in which receptors for the tumouricidal lipids are inactivated or deleted to produce a tumouricidal lipids are inactivated or deleted to produce a tumouricidal induced population activated immunocytes to the host), producing a tumour associated lipids to context APCS, in which reappores for the tumouricidally activated or deleted to produce a tumouricidally activated or functionally deartivated to produce a tumouricidally activated or functionally deartivated to produce a tumouricidally activated or context or produce a tumouricidally activated or colls to be host, or allowing a superanticidally activated or colls to be the host, or allowing a superanticidally activated or colls to produce a tumouricidally activated or cells to be the host, or tumouricidal or cell population in vivo in a mammal (by administ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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242 RESLSFYISLNDE 254

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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces

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230 RESIASYLSLTSE 242

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The invention relates to a novel method for identifying a compound that modulates T lymphocyte activation. The method comprises contacting a T cell comprising an A-raf-1 or TCPTP/PPTN2 polypeptide with a compound, where the A-raf-1 or TCPTP/PPTN2 polypeptide his a compound, where the A-raf-1 or TCPTP/PPTN2 polypeptide by a mucleic acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, surface marker expression, cytokine production, antibody production, corpilaraty cells. The A-raf-1 or TCPTP/PTN2 proteins may be used as drug targets for compounds that suppress or activate lymphocyte activation and migration, eag. for the treatment of diseases in which modulation of the immune response is desired such as delayed type hypersensitivity reactions, athima, allergies, graft versus host disease, and activated for treatmng disorders related T and B cell activation and migration early sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with
                                                                                                                                                                                                                         immunosuppressive, antiasthmatic; antiallergic; antiinflammatory; lymphocyte activation; lymphocyte migration; cytokine production; cell surface marker expression; antibody production; apoptosis; allergy; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity; graft versus host disease; inflammation; Src-like-adaptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pardo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 72; 126pp; English.
                                       ABR59698 standard; protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masuda E,
                                                                                                                                                                                                     Human; T lymphocyte activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2002; 2002WO-US031618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2001; 2001US-0327212P
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIGE-) RIGEL PHARM INC
                                                                                                                                                              Human Src-like-adaptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-363276/34.
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                                                                                                                                                                                                                                                                                                                                                                                         WO2003029277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li C,
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                       25-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compound
                                                                                ABR59698;
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RESULT 13
                     ABR59698
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and artagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tenden and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

AMUS9510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                    128
                                                                                                                                                   119 FYSLSVR-----HRQVKHYRIFRLPNNWYXISPRLTFQCLEDLVNHYSEVADGLCCVLT 172
                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                              6 KSTPAPA-----ERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLRVISDEGGW
                                                    69 WTVLSEVSGREYNIPSVHVGKVSHCWLYEGLSREKAEELLLLPGGNPGGAFLIRESQTRRG
                                                                                                                             SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLK
                                                                                                                                                                                                        189 EPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSBAATG-----ESSLLSEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vaccination; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                AAU31072 standard; protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted protein #1563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 399; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-2001; 2001WO-US008656
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                                                                                                                                                                                                                                                                                 RESLSFYISLNDE 254
                                                                                                                                                                                                                                                                                                                     230 RESIASYLSLTSE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179449-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU31072;
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23;

Length 276; Indels

DB 6; 85;

35.6%; Score 481.5; DB 6 40.3%; Pred. No. 1.1e-40; tive 43; Mismatches 85

Query Match Best Local Similarity 40.3% Matches 102; Conservative

(ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences

blood data

Sequence 315 AA;

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QTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDI 183
                                                                                                                                                                                                                             PGKKKEMGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLRVISD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
                                                                                                                         PSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSE
                                                                                                                                                                                                             CCLLKEPCVLORAGPLPGKDIPLPVTVQRTPLNWKBLDSSLLFSEAATGE-----ESLLS
                                                                                                     65 DGDWWTVLSEVSGREYNIPSVHVGKVSHG-WLYEGLSREKAEELLLLPGNPGGAFLIRES
                                                                                                                                                                          153 ETKKGFYSLSVR-----HRQVKTYRIFRLPNNWYYISPRLFFQCLEDLVNHYSBVADGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilincal vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder.
                          Gaps
                          13;
 DB 4; Length 315;
                          Indels
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Match 34.8%; Score 470.5; DB 4; Local Similarity 39.3%; Pred. No. 1.8e-39; es 103; Conservative 46; Mismatches 100;
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MEHRABAN F.
CONLEY P B.
TOPPER J N.
LAW D.
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N-PSDB; ABQ98669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORF476
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Query Match
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The present invention relates to novel human ORFX polypeptides and their

Claim 10; SEQ ID NO 952; 78pp; English.

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coding sequences (ABP63631-ABP64681 and ABQ98194-ABU992e). The sequence were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HVWEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX associated disorder, e.g. cancer, actdiovascular disease, allergy, autoimmune disease, wound healing, bloo coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was sequence in electronic format directly from the USPTO web site at sequence.html?DocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGSLPSRRKSLPSPSLSSSVQGQGPVTIMEAERSKATAVALGSFPAGGPAELSLRLGEPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGSLPSRRKSLPSPSLSSSVQGQGPVTWEAERSKATAVALGSFPAGGPAELSLRLGEPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI
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                                                                                                                                                                                                                                                                                                                                                        'Match 33.4%; Score 452.5; DB 5; Length 96; Local Similarity 76.8%; Pred. No. 2.1e-38; les 96; Conservative 0; Mismatches 0; Indels 29
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completed: February 20, 2004, 09:29:40 Ne : 97 secs time Search Job tim

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protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - human N;Contains: protein-tyrosine kinase lyn, splice form B C;Species: Homo sapiens (man) C;Date: 11-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Feb-2000 C;Accession: A26719; D38268; PH0949; I53715 R;Yamanashi, Y.; Fukushige, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.; )
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.5%; Score 493.5; DB 2; Best Local Similarity 43.6%; Pred. No. 2.1e-33; Matches 115; Conservative 38; Mismatches 82;
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C,Superfamily: SH3 homology; SH2 homology
F;29-77/Domain: SH3 homology cSH3>
F;84-175/Domain: SH2 homology cSH2>
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30	290	21.4	206	Н	824553		
31	286.5	21.2	557	-	TVFVS2	a	
32	286.5	21.2	587	Н	TVFVPR	protein-tyrosine k	
33	284.5	21.0	533	Н	TVCHS	protein-tyrosine k	
34	284.5	21.0	568	Н	TVFVS1	protein-tyrosine k	
35	279.5	20.7	526	ч	TVFV60	protein-tyrosine k	
36	276	20.4	509	-	TVHAST	protein-tyrosine k	
37	275	20.3	546	N	S52314	protein-tyrosine k	
38	274.5	20.3	532	н	B34104	protein-tyrosine k	
39	273.5	20.2	526	-	TVFVR	protein-tyrosine k	
40	273.5	20.2	526	N	S15582	protein-tyrosine k	
41	273.5	20.5	542	Н	TVHUSC	protein-tyrosine k	
42	273	20.5	545	N	S52313	protein-tyrosine k	
43	272	20.1	541	н	A43610	protein-tyrosine k	
44	271.5	20.1	532	Н	A34104		
45	269.5	19.9	526	N	\$26420	protein-tyrosine k	
					ALIGNMENTS		
RESULT 1							
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C; Species: Mus musculus (house mouse)	SS: Mus r	musculu	s (hous	e e			
C; Dare:	US-Dec-	ביים לונה מיינו	sequence_revision	r.	08-Dec-1995	#text_change 12-Feb-1999	
C, Access	STORE AD	701/	÷ ;	5	>		
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A, Title:	Charact	terizat	ion of	, c	c-like adapter	otein that associates wit	끉
A, Refere	ence num	ber: A5	7152; M	dip	43; PMID: 75438	98	
A; Access	ion: A5'	7152					
A;Status	A;Status: preliminary;	ninary;	not co	mpa	compared with conceptual translation	nslation	
A;Molecule	le type	type: mRNA	٠				
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9 KSLPSPS---LSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 6 KSTSPPSERPLSSS-----EGLESDFLAV-LIDYPSSDISPPIFRGEKLRVISDE GDWWTVLSEVSGREYNI PSVHVGKVSHGWLYEGLSREKAEELLLLLPGNPGGAFLIRESQT

125 115 185 169 236

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126 RRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICC

LLKEPCVLQR-----AGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG----EESL

186

LSEGLRESLSFYISL-NDEAVSLD 259

237

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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A,Gross-references: GB:L14823; NID:2294580; PIDN:AAA20945.1; PID:2294581
A,Note: in Genbank entry RATIVNETYR, release 116.0; PIDN:AAA20945.1, the source is design, N.Note: in Genbank entry RATIVNETYR, release 116.0; PIDN:AAA20945.1, the source is design, S.S.12/Product: protein-tyrosine kinase erc; protein kinase homology; SH3 homology ships and the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the source of the s
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N;Contains: protein-tyrosine kinase lyn, splice form B
N;Contains: protein-tyrosine kinase lyn, splice form B
C;Species: Ratuus norvegicus (Norway rat)
C;Decies: Ratuus norvegicus (Norway rat)
C;Decies: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: IsG160; IG7811; IG7812
R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.
J; Immunol. 150, 222, 1993
A;Title: Bacterially expressed rat p561yn binds several proteins in rat basophilic leuke
A;Reference number: I56160
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A;Molecule type: mENA,
**Residues: 1-230, 'L',232-307,'A',309-418,'Y,'420-512 <RIDI>
A;Residues: 1-230,'L',232-307,'A',309-418,'Y,'420-512 <RIDI>
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A;Note: in Genbank entry RAILYNATYR, release 116.0, PIDN:AAA20944.1, the source is design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <mINA
A;Cross-references: GB-L14951; NID:G294582; PIDN:AAA41549.1; PID:G294583
A;Cross-references: GB-L14951; NID:G294582; PIDN:AAA41549.1; PID:G294583
A;Cross-references: GB-L14951; NID:G294582; C.
Gene 138, 219-222, 1994
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed
A;Reference number: 153715; MUID:94171041; PMID:B125304
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Molecule type: mRNA
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Hesches: 169-424 «PAR»
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Heschiques: 169-424 «PAR»
Heschiques: 180-11409, 180-11409, 1992
Hittle: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobly Reference number: PH0949; MUID:92378604; PMID:1510669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: mRNA
A, Rosidues: 369-424 (BIE>
A, Residues: 369-424 (BIE>
A, Residues: 369-424 (BIE>
A, Raben, N.; Miller, L.; Jelsema, C.
Gene 138, 219-222, 1994
A, Title: The CDNAs encoding two forms of the LYN protein tyrosine kinase are expressed
A, Reference number: 153715, MUID: 94171041; PMID: 8128304
A, Recession: 153715
A, Scratus: preliminary; translated from GB/EMBL/DDBJ
A, Rosidues: 1-24,46-512
A, Rosidues: 1-24,46-512
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A, Gene: GDS: LYN
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                                            encodes a possible tyrosine kinase similar PMID:3561390
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                                                                                                                                           A;Accession: A26719
A;Nolecule type: man.
A;Rosidues: L-512 <x2AM>
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A;Cross-references: GB:MID:g187268; PIDN:AAA59540.1; PID:g307144
B;Partanen, J.; Mackelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
B;Partanen, J.; Mackelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
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A,Cross-references: GDB:120159; OMIM:165120
Mol. Cell. Biol. 7, 237-243, 1987
A; Title: The yes-related cellular gene lyn
A; Reference number: A26719; MUID:87172710;
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                                                                                                                                                                 38 SNKQQRPVPE-SQLLPGQRFQAKDPEEQGDIVVALYPYDGIHPDDLSFKKGEKMKVLEEH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse N;Contains: protein-tyrosine kinase lyn, short splice form C;Species: Was musculus (house mouse) C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 03-Mar-2000 C;Accession: A39719; B39719; B39750;
                                                                                                                                                                                                                             66 GDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIR
                                                                                                                 6 SRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED
                                                           Gaps
                                                        9
27.2%; Score 367.5; DB 1; Length 512; 40.3%; Pred. No. 1.2e-22; ive 33; Mismatches 78; Indels 9.
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"Supeription: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP G. Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 hc C. Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 hc C. Severates: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos F; 2-505/Product: protein-tyrosine kinase hck #status predicted «NAT» P; 2-505/Product: protein-tyrosine kinase hck #status predicted «NAT» P; 213-220/Domain: SH3 homology «SH3» P; 213-220/Domain: protein kinase homology «KIN» P; 213-2497/Domain: protein kinase ATP-binding motif P; 247-255/Region: protein kinase ATP-binding motif P; 25/Region: protein kinase ATP-binding motif P; 25/Region: protein kinase ATP-binding motif F; 25/Region: protein kinase ATP-binding motif F; 25/Region: protein kinase ATP-binding motif F; 25/Region: myristylated amino end (Gly) (in mature form) #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Active site: Lyg #status predicted F; 25/26%/Ac
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1505 < ZIE>
A; Cross-references: GB:MI6592; NID:g183913; PIDN:AAA52644.1; PID:g306833
A; Cross-references: GB:MI6592; NID:g183913; PIDN:AAA52644.1; PID:g306833
A; Firal detaky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H.
A; Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase
A; Reference number: JC1149; MJID:92241680; PMID:1572549
A; Accession: JC1149
A; Accession: JC1149
A; Cross-references: EMBL:X59741
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C;Species: Rattus norvegicus (Norway rat).
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: UQ1321; S18974
R;Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
Biochan, Biophys. Res. Commun. 181, 1137-11144, 1991
A;Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
A;Reference number: UQ1321; MUID:92109719; PMID:1764064
                                                                      Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells Reference number: A27812; MUID:87257943; PMID:3453117 Accession: A27812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic acid sequence not shown; not compared with conceptual translation
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A; Residues: 1-24,46-56,7°7,78-160,1'1,162-278,'L',280-390,'I',392-424,'D',426-512 < YI2>
A; Residues: 1-24,46-66,7°7,78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 < YI2>
A; Cross-references: Gsim75697; NID:9198942; PIDN:AAA39472.1; PID:9198943
C; Superfamily: protein-tyrosine kinase topotein blocked amino end; lipoprote C; Reywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote F; 1-22, Froduct: protein-tyrosine kinase lyn, long splice form #status predicted < MATL> F; 1-24,46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted < F; 70-118/Domain: SH3 homology < SH3>
F; 225-50/Domain: SH3 homology < SH2>
F; 225-60/Domain: protein kinase Amology < KIN>
F; 252-261/Region: protein kinase Amology < KIN>
F; 252-261/Region: protein kinase Ample-binding motif F; 275/Active site: myristylated amino end (GIY) (in mature form) #status predicted F; 275/Active site: Lys #status predicted files: Amino end (GIY) (in mature form) #status predicted files: Amino end (GIY) (in mature form) #status predicted files: Amino end (GIY) (in mature form) #status predicted files: Amino end (GIY) (in mature form) #status predicted files: Amino end (GIY) (in mature form) #status predicted files: Amino end (GIY) (in mature form)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred
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R;Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R. Mol. Cell. Biol. 11, 339-3406, 1991
A;Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
A;Reference number: A39719; MUID:91260688; PMID:1710766
A;Accession: A39719
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A;Residues: 1-505 <QUI>
A;Cross-references: GB:M16591
A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-76,'F',78-160,'I',162-278,'L',280-390,'I',392-424,'D',426-512 <YII>
A;Cross-references: GB:M57696; NID:g198940; PIDN:AAA39471.1; PID:g198941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIR 121
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A; Mesidues: 1-24,46-512 <5TA2>
A; Mesidues: 1-24,46-512
A; Cross-references: GB: M64609
R; Yi, T.; Bolen, J.S.; Ihle, J.N.
R; Yi, T.; Bolen, J.S.; Ihle, J.N.
A; Yitle: Hematopoletic cells express two forms of lyn kinase differing by
A; Reference number: A39750; MUID:91203857; PMID:2017160
                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-512 <STA1>
A;Cross-references: GB:M64608; NID:g198938; PIDN:AAA39470.1; PID:g198939
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qq à 입 ð g 8 form) #status predicted

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F_j 2/Modified site: myristylated amino end (Gly) (in mature F_j 269/Active site: Lys \#status predicted
                                                                                                Query Match
Best Local Similarity
Matches 75; Conserv
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A;Status: preliminary
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-50, V',52-204, R',206-305, T',307-503 <REM>
A;Cross-references: EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID:g57582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: hck
C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2
C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related t
                                                                                                    A;Cross-references: GB:S74141; NID:g241436; PIDN:AAB20754.1; PID:g241437
A;Experimental source: megakaryocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGSLPSR--RKSLPSPSLSSSVQGQGPVTME-----
                                                                                                                                                             R.Rema, V.; Swarup, G.
submitted to the EMBL Data Library, December 1991
A.Reference number: S18974
                                   A, Molecule type: mRNA
A, Residues: 1-503 < OKA>
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F121-218/Domain: Drotein Kinase bomology <KIN>
F237-495/Domain: protein Kinase homology <KIN>
F245-253/Region: protein kinase ATP-binding motif
F245-253/Region: protein kinase ATP-binding motif
F12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F12/Modified site: palmitate (Cyp) (covalent) #status predicted
F126/Active site: Lys #status predicted
F1388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
                                                                         7
                                                                                                                                                                                         51 PPDEHLDEDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSLVTGREGYVPS 110
                                                                                                                                                                                                                                                                                         85 VHVGKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPA 140
                                                                                                                                                                                                                                                                                                                                               111 NFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLIRESETNKGAFSLSVK-DVTT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NiAlternate names: kinase-related transforming protein (bmk)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A27282, A39973
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Fitle: Nucleotide sequence of the mouse hck gene.
A;Reference number: A27282; MUID:88067781; PMID:3684607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VPDPTSSSKLGPNNSNSMPPGFVEGSEDTIVVALYDYEAIHREDLSFQKGDQMVVLEEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 DWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LPSPSLSSSVQGQGPVTME---AERSKAT-AVALGSFPAGGPAELSLRLGEPLTIVSEDG
                                                                                                                                                  25 PVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:g309118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Modecule type: mRNA
A; Residues: 1-503 «KLE»
A; Cross-references: GS-1209; PIDN:CAA68544.1; PID:g51210
A; Cross-references: GS-1200; M.D.; Dunn, A.R.
F; Holtzman, D.A.; Cook, W.D.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
A; Title: Isolation and sequence of a cDNA corresponding to a src-relate
A; Accession: A39973; MUID:88068587; PMID:3317404
                                                                                                                                                                                                                                                                                                                                                                                                                                    141 SWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 QGELIKHYKIRCLDEGGYYISPRITFPSLQALVQHYSKKGDGLCQRLTLPCV 221
                                                                         ر.
دی
       Length 505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 status: preliminary, not compared with conceptual translation; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels
                                                                         Indels
26.1%; Score 352.5; DB 2; 43.6%; Pred. No. 2.1e-21; iive 24; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.0%; Score 352; DB 1;
41.0%; Pred. No. 2.3e-21;
live 33; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (BC 2.7.1.112) hck
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Best Local Similarity 41.0%
Matches 82; Conservative
                                                                             Conservative
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16:44:51

70

Feb

Fri

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A'Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP c'Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 howely autophosphorylation; blocked amino end; lipoprotein; myristylation; phos F;2-509/Product: protein-tyrosine kinase lck #status predicted «MAT> F;2-7224/Domain: SH3 homology «SH3> F;27-224/Domain: SH2 homology «SH2> F;243-501/Domain: protein kinase homology «KIN> F;243-501/Domain: protein kinase ATP-binding motif F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted F;33/Active site: Lys #status predicted F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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A.Residues: 1-35 c.PaKs.
A.Residues: 1-35 c.PaKs.
A.Residues: 1-35 c.PaKs.
A.Residues: 1-35 c.PaKs.
B.Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.
Mol. Cell. Biol. 8, 3058-3064, 1988
A.Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell
A.Reference number: 157636, MUID: 89096891; PMID: 2850479
                                                    A;Residues: 1.86, 'P', 88-509 <PER>
A;Cross-references: EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID:g34295
B;Koga, Y.; Caccia, N; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.
Bur. J. Immunol. 16, 1643-1646, 1986
A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homol A;Reference number: S07200; MUID:87133831; PMID:3493153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-205, ASAITPI',212-257, 'RCGW',262,'TTT',266,'T',268-281,'AGRLP',287-503,'ST}
A; Cross=references: EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID:g36808
R; Vaillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 368-471, 'H',473-509 <VEI>A,Coss-references: BMBL.X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289
A;Cross-references: EMBL.X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289
R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.
Biochim. Biophys. Acta 888, 286-295, 1986
A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).
A;Reference number: S07143; MUID:87000726; PMID:3489486
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A;Map position: 1p35-1p34.3
A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1
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A; Residues: 1-35, 'VR'
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F; 218-214/Domain: SH3 homology SH3>
F; 218-2491/Domain: protein kinase homology KIN>
F; 218-2491/Domain: protein kinase homology KIN>
F; 218-2491/Apkagion: protein kinase ATP-binding motif
F; 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F; 263/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            blk, in B lymphoid cells.
                                                                                                                                                                                                                                                                                                                                                                                                            procession: Atnase (EC 2.7.1.112) blk [validated] - mouse C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Accession: A40092
R.Dymecki, S.M.; Niederbuber, J.E.; Desiderio, S.V. Science 247, 332-336, 1990
A.Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells A. Reference number: A40092; MUID: 90117147; PMID: 2404338
A. Accession: A40092; MUID: 90117147; PMID: 2404338
A. Accession: A40092; MUID: 90117147; PMID: 2404338
A. Residues: 1-499 < DYM>A. Residues: 1-499 < DYM>A. Residues: 1-499 < DYM>A. Residues: 1-499 < DYM>A. Gross-references: GB: M30903; NID: 922076; PIDN: AA40453.1; PID: 9202077
C. Genetics: MGI: Blk
A. Cross-references: MGI: 88169
A. Map position: 14:28.0
C. Superfamily: protein-tyrosine kinase src; protein kinase homology C. Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylat F. F. S-107/Domain: SH2 homology < SH3>F: 118-214/Domain: SH2 homology < SH3>F: 118-214/Domain: protein kinase App-binding motif F: 241-249/Region: protein kinase App-binding motif F: 241-249/Region: protein kinase App-binding motif F: 241-249/Region: protein kinase App-binding motif F: 241-249/Region: myristylated amino end (Gly) (in mature form) #status predict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TMEAERSK 34
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36.0%; Pred. No. 9.5e-21;
cive 32; Mismatches 73
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                                                                               10 LCQKLSVPCV---SPKPQK 225
183 ICCLLKEPCVLQRAGPLPGK
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Matches 80; Conservative
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A; Molecule type: mRNA
A; Residues: 1-88 cCHGO.
A; Cross-references: GB:M85043
A; Experimental source: thymus, spleen
A; Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
A; Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)
B; Strebbardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 9778-9782, 1987
A; Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related
A; Reference number: A39939; MUID:88097370; PMID:3321053
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A, Residues: 52-507 <STR>
A, Rosidues: 52-507 <STR>
A, Cross-references: GB:003579; NID: g212712; PIDN: AAA49081.1; PID: g212713
C; Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 hc
C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho:
F; 66-114/Domain: SH3 homology <SH3>
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F;241-499/Domain: protein kinase homology <KIN>
F;241-499/Domain: protein kinase APP-binding motif
F;249-257/Region: protein kinase APP-binding motif
F;27/Modified site: myristylated amino end (G1y) (in mature form) #status predicted
F;392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken
NyAlternate names: kinase-related transforming protein (tkl); T-cell surface antigen associated special surface antigen associated special surface antigen associated special surface antigen associate is delugable surface.
C; paces: Gallua 2010 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
C; Accession: A42126; A39939
R; Chow, L. M.; Ratciliffe, M.J.; Veillette, A.
Mol. Cell. Biol. 12, 1226-1233, 1992
A; Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
A; Reference number: A42126; MUID:92186654; PMID:1545804
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C;Species: Torpedo californica (Pacific electric ray)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 18-Feb-2000
C;Accession: B49114
R;Swope, S.L.; Huganir, R.L.
A;Title: Molecular cloning of two abundant protein tyrosine kinases in Torpedo electric A;Reference number: A49114; MUID:94043386; PMID:8227079
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     119 LIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSE
                                                         38 VALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKVS----HG
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                                                                                                                                                                                                                                                            212 ASDGLCTKLSRPCQTQK 228
                                                                                                                                                                                             179 LADDICCLLKEPCVLQR 195
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A/Residues: 1-11 < VOR.

A/Residues: 1-11 < VOR.

A/Residues: 1-11 < VOR.

A/Residues: 1-11 < VOR.

B/Gross-references: GBH.18098, NID:9198766; PIDN:AAA39421.1; PID:9198767

B/Gross-references: GBH.18098, NID:9198766; PIDN:AA39421.1; PID:9198767

A/Residues: 157636; MUID:99096891; PMID:2850479

A/Recession: 177452

A/Residues: 177452

A/Residues: 1-35, VR.

A/Residues: 1-35, VR.

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A/Residues: 1-35, VR.

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A/Residues: 1-35, VR.

A/Residues: 1-35, VR.

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A/Residues: 1-35, VR.

A/Residues: 1-35, VR.

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A/Residues: 1-35, VR.

A/Residues: 1-35, VR.

A/Res
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C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Accession: I48845; A2339; I57629; I77452
R, Voronova, A.F.; Setton, B.M.
Nature 319, 682-685, 1986
A, Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote
A, Reference number: 148845; MUID:86146842; PMID:3081813
A, Reference number: 148845, MUID:86146842; PMID:3081813
A, Residues: 1509 < VOR1>
A, Residues: 1509 < VOR1>
A, Molecule type: mRNA
A, Residues: 1509 < VOR1>
A, Molecule type: mRNA
A, Residues: 1509 < VOR1>
A, Accession: A3339; MID:354813; PIDN:CAA27234.1; PID:354814
R, Marth, J.D.; Peet, R.; Krebs, E.G.; Perimutter, R.M.
Cell 43, 393-404, 1985
A, Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres
A, Reference number: A23639; MUID:86079521; PMID:2416464
A, Accession: A23639
A, Molecule type: mRNA
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Accession: A23639
A, Molecule type: mRNA
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 288-509 < VARE>
A, Residues: 1-282, VVP, 282-509 < VARE>
A, Residues: 1-282, VVP, 282-509 < VARE>
A, Residues: 1-282, VVP, 282-509 < VARE>
A, Residues: 1-282, VVP, 282-509 < VARE>
A, Residues: 1-282, VVP, 282-509 < VARE>
A, Resid
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GETPENFVAKANSLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVR 168
                                                                                                                                                   LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
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                                                                                                                                                                                                                                 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK
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%Status: preliminary: translated from GB/EMBL/DDBJ
A,Moleoule type: DNA
A,Residues: 1-11 <VOR>
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les 77; Conservative
                                                                                                                                                   136
                                                                                                                                                                                                                                            169
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A45201

Partice Tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog

NiAlternate names kinase (EC 2.7.1.112) yes [similarity] - African clawed frog

C,Species: Xenopus laevis (African clawed frog)

C,Species: Xenopus laevis (African clawed frog)

C,Species: Xenopus laevis (African clawed frog)

C,Species: Xenopus laevis (African clawed frog)

C,Species: I. 223-233, 1989

A,Steele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.

A,Feference number: A45501

A,Accession: A45501

A,Accession: A45501

A,Accession: A45501

A,Accession: A45501

A,Accession: A45501

A,Accession: A45501

A,Reference number: 808517

A,Accession: BMBLA377

R,Scele, R.E.; Irwin, M.Y.; Knudsen, C.L.; Collett, J.W.; Fero, J.B.

A,Reference number: 808517

A,Reference number: 808517

A,Reference number: 808517

A,Reference number: 808517

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A,Reference number: 808517

A,Reference number: 
                         171 IFLVRESETTKGAYSLSIR----DWDEVRGDNVKHYKIRKLDNGGYYITTRAQFESLQK 225
                                                                                                                                                         226 LVKHYREHADGLCHKLTTVCPTVKPQTQGLAKDAWEIPRESLRLEVKLGQGCFGEVWMGT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VALYDYBARTTEDLSFRKGERFQIINNTEGDWWEARSIATGKTGYIPSNYVAPADSIQAE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 GWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIR----H 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 YRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPC------VLQRAGP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 YKIRKLDNGGYYITTRAQFESLQKLVKHYSEHADGLCYRLTTVCPTVKPQTQGLAKDAWE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 IPRESLRIDVALGQGCFGEVWIGTWNGTTKVAIKTLKPGTMMPEAFLQBAQIMKKLRHDK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 LPGKDIPLPVTVOR------TPLNWKELDSSLLFSEAATGEESLLSEGLRES 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 VALGSFPAGGPAELSLRLGEPLTIVSE-DGDWWTVLSEVSGREYNIPSVHVGKV----SH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 23.6%; Score 319.5; DB 1; Length 537; 1 Similarity 33.2%; Pred. No. 1.2e-18; Score 39; Gaps 84; Conservative 38; Mismatchee 92; Indels 39; Gaps
                                                                                                                                                                                                                          213 ----TPLNWKELDSSLLFSEAATGEESLLSEGLRESL-SFYISLNDEAV 256
                                                                                                                                                                                                                                                           286 WNGTTKVAIKTLKLGTMMPEAFLQEAQIMKKLRHDKLVPLYAVVSEEPI 334
                                                                                           172 LVDHYSELADDICCLLKEPC-----VLORAGPLPGKDIPLPVTVOR--
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Rikitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.
Nature 297, 205-208, 1982
A;Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its transf
A;Reference number: A00633; MUID:82195528; PMID:6281656
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C;Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; tran
F;88-137/Domain: SH3 homology <SH3>
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F;273-281/Region: protein kinase ATP-binding motif
F;255/Active site: Lys #status predicted
F;416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGASSSFSAVPSP-YPSTLTGGGTV-----FVALYDYBARTTDDLSFKKGERFQI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 SLTSRVGGVTGGVTM-----FIALYNYDARTEDDLTFRKGEKFHIINSSEGDWWEAR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 SEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 SLTTGSTGYIPSNYVAPVDSIQAEEWYFGKMGRKDTERMLLCPGNPRGTFLIRESETTKG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VSE-DGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKARELLLLPGNPGG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 INNTEGDWWEARSIATGKTGYIPSNYVAPADSIQABEWYFGKMGRKDAERLLLINPGNQRG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AFLIRESQIRRGSYSLSVRLSRPASWDRIR-----HYRIHCLDNGWLYISPRLTFPSLQA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SLSSSVQG-QGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIV-SEDGDWWTVL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73
C;Species: avian earcoma virus Y73
A;Note: host Gallus Gallus (chicken)
C;Date: 27-Nov-1965 #sequence_revision 27-Nov-1965 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 31.5%; Pred. No. 1.1e-18;
91; Conservative 43; Mismatches 105; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ilarity 41.0%; Pred. No. 4.3e-19;
Conservative 27; Mismatches 67; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.7%; Score 320; DB 1; Length 528; 31.5%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: genomic RNA
A;Residues: 1-528 <KIT>
C;Comment: This protein is synthesized as a gag-yes polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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nes 75; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 EPC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 VPC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A00633
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 20, 2004, 08:16:06; Search time 39 Seconds (without alignments) 348.469 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-939-853A-75 1353 1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA 261

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	3h6q3 homo sapien	manm (59622 rattus norv	~	13239 homo sapien	3 homo	mus m	_	_	macac	51451 homo sapien	mus m	50545 rattus norv	~	P06239 homo sapien	mus m	gallus g	~	s xenor	-41	I homo	7 homo	э рошо	7 xipho	ın	00527 avian sarco	9 mus	ï	46 xiph	4.	2977 gallus	8923 canis f	5876
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;	DI	SLA2_HUMAN	SLA2 MOUSE	SLA1_RAT	SLA1 MOUSE	SLA1 HUMAN	LYN HUMAN	LYN MOUSE	LYN RAT	HCK_HUMAN	HCK_MACFA	BLK HUMAN	HCK_MOUSE	HCK_RAT	BLK_MOUSE	LCK_HUMAN	LCK MOUSE	LCK_CHICK	SR42 DROME	YES XENLA	YES CHICK	FYN HUMAN	YES HUMAN	FGR_HUMAN	YES XIPHE	FYN XENLA	YES_AVISY	FYN MOUSE	YES MOUSE	FYN XIPHE	FGR MOUSE	YRK_CHICK	YES CANFA	FYN CHICK
1	08	Н	Н	Н	Н	ч	٦	Н	Н	Н	М	Н	Н	Н	Н	Н	н	Н	ч	Н	~	H	Н	Н	ч	Н	Н	Н	ч	Н	٦	Н	,	Н
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	Match				•				•			•	-			4	•				•			•			•		•	•		2.2	•	•
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P42690 spongilla l	P00525 avian sarco	P00523 gallus gall	P00528 drosophila	P14085 avian sarco	P15054 avian sarco	P14084 avian sarco	Q9wd9 rattus norv	P00524 rous sarcom	P12931 homo sapien	 P17713 hydra atten 	P13116 xenopus lae
SRK4 SPOLA	SRC AVISR	SRC_CHICK	SR64 DROME	SRC AVIST	SRC_AVIS2	SRC_AVISS	SRC RAT	SRC_RSVSR	SRC_HUMAN	STK_HYDAT	SRCZ_XENLA
гH	H	~	-	Н	н	ч	Н	Н	-	Н	-
909	526	532	552	557	587	568	535	526	535	509	531
21,4	21,2	21.2	21.2	21.2	21,2	21.0	20.5	20.4	20.4	20,4	20.3
290	286.5	286.5	286.5	286.5	286.5	284.5	277.5	276.5	276.5	276	274.5
34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 SLAZ HUMAN ID 201222 DAT 10-0C DB STAT 1 10-0C DB STAT 1 10-0C DB STAT 1 STAT 1 RE STAT 1 RE STAT 1 RE SEQUE RE MADDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE MEDIA RE SEGUE RE MEDIA RE MEDIA RE MEDIA RE SEGUE RE MEDIA RE SEGUE RE S
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MEDINE-2538825; PubMed=12477932; MEDINE-2538825; PubMed=12477932; MEDINE-2538825; PubMed=12477932; MEDINE-2538825; PubMed=12477932; MEDINE-2538825; PubMed=12477932; Magner L., Shemmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Perer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Andan A., Young A.C., Shevchenko Y., Bouffard G.G., Shenting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abramson M.C., Shevinguez A. C., Grimwood J., Schmutz J., Whers R.M., Matan M., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Rodziguez S., Sanchez M., "Goneration and initial analysis of more than 15,000 full-length human mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002). Pandey A. Idearcha.

A Constantinescu S.N., Ohara O., Sawasdikosol S., Lodish H.F., Mann M.,

Tonstantinescu S.N., Ohara O., Sawasdikosol S., Lodish H.F., Mann M.,

Tonstantinescu S.N., Ohara O., Sawasdikosol S., Lodish H.F., Mann M.,

Tonoteln-2 (SLAP-2), which negatively regulates T cell receptor

T signaling.";

J. Biol. Chem. 277:19131-19138 (2002)

- PUNCTION: Adapter protein, which negatively regulates T-cell

receptor (TCR) signaling. Inhibits T-cell antigen-receptor induced activation of nuclear factor of activated T-cells. May act by

linking signaling proteins such as ZAP70 with CBL, leading to a climital along signaling proteins.

- SUBUNIT: Interacts with phosphorylated proteins ZAP70 and CD3Z via its SH2 domain (By similarity). Interacts with phosphorylated CBL

- SUBCELLULAR LOCATION: Cytoplesmic. Isoform I is localized to the endosomal vesicles, including late endosomal vesicles. including late endosomal vesicles. Isoform 2 may be cytoplasmic and is not Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
A Huckle E., Hunt S.E., Jeksech K., Johnson C.W., Johnson D.,
Kay M.P., Kimberley A.M., King A., Kinghts A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
A Marsh V.L., Martin S.L., McConnachle L.J., McLay K., McMarray A.A.,
Milne S.A., Mistry D., Moore M.J.F., Mullkin J.C., Nickerson T.,
A Diliance B.J.C.T., Parchalingam S.R., Plumb R.W., Ramesy H.J.,
A Rice C.M., Scott C.E., Sehra H.K., Showhken R. Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
A Kace C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
A Tracey R.M., Toomans A.C., Vaudin M., Wall M., Wallis J.M.,
Thorpe A.,
Milning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J. "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001). Name=1; Synonyms=p28; IsoId=Q9H6Q3-1; Sequence=Displayed; Note=Isoform 3 is produced by alternative initiation at Met-27 of isoform 1; localized to membranes. ALTERNATIVE PRODUCTS: Event≈Alternative splicing; Named isoforms≈2; MEDLINE=22013997; PubMed=11891219; SEQUENCE FROM N.A. CHARACTERIZATION

ame=2; Synonyms=p23, SLAP-2-v, MARS-v; IsoId=09H6Q3-2; Sequence=VSP 007240, VSP 007241; Note=Isoform 4 is produced by alternative initiation at Met-27 of isoform 2;

Event *Alternative initiation;

Н 260 HSSP; P06239; 1LKK 210 ႕ 27 31 93 194 INIT MET DOMAIN DOMAIN LIPID VARSPLIC SEQUENCE VARSPLIC MUTAGEN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-myristoyl glycine (By similarity).
LADDICCLLKEPCVLQRAGPLPGKDIPLPVTV -> GWPAP
WQGYTPTCDCAEDTTQLERAGQLPPVF (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FIId=VSP 007240.
Missing (in isoform 2).
FIId=VSP 007241.
G-AR. ABOLISHES LOCALIZATION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.2%; Score 1342; DB 1; Length 260; 99.6%; Pred. No. 3.7e-105; Live 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR ISOFORM 3 AND ISOFORM 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AA; 28454 MW; A402C03449261B3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLA C-TERMINAL.
                                                                                                                                                                                                                                                               EMBL; AF326353; AAL29204.1; --
EMBL; AF290985; AAL38197.1; --
EMBL; AF290986; AAL38198.1; --
EMBL; AK025645; BAB15201.1; --
EMBL; AL031667; CAC44645.1; ALT_TERM.
EMBL; AL0503.18; CAB75565.1; --
EMBL; BC042041; AAH42041.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
ProDom; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6%
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:17329; SLA2.
MIM; 606577; -.
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CENTELLE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=CS7BL/6J, and NOD; TISSUE=Retina, and Thymus;

XX MEDINE=2534683; PubMed=12466851;

XA STRAIN=CS7BL/6J, and NOD; TISSUE=Retina, and Thymus;

XX NEADAN X. Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

XX Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,

XX Andarelli R., Hill D.P., Bult C., Hume D.A., Chackenbush J.,

Baldarelli R., Bradt D., Brusic V., Chothia C., Corbubah J.,

Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.S., Cousins

A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Basterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

A Gasterland T., Gariboldi M., Gissi C., Godzik R., Gough J.,

A Grimmond S., Gustincich S., Hirokawa N., Jackeon I.J., Jarvis E.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Redzierski R.M., King B.L.,

A Magoht D.R., Maltais L., Marchionni L., Morkenzie L., Miki H.,

Netrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

A Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

A Sandelin A., Yaylor M.S., Taylor M.S., Teasdale R.D., Tomita M.,

Verardo R., Wapner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
                      VSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIR 120
                                                                     ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, MYRISTOYLATION, INTERACTION WITH CBL; ZAP70 AND CD3Z, AND MUTAGENESIS OF GLY-1; PRO-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pandey A., Ibarrola N., Kratchmarova I., Fernandez M.M., Constantinescu S.N., Ohara O., Sawasdikosol S., Lodish H.F., Mann M., "A novel Src homology 2 domain-containing molecule, Src-like adapter protein-2 (SLAP-2), which negatively regulates T cell receptor
                                                                                                                                                                                              DICCLIKEPCVLQRAGFLFGKDIFLFVTVQRTFLNWKELDSSLLFSEAATGEESLLSEGL
                                                                                                            ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELAD
                                                                                                                                                              DICCLLKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATGEESLLSEGL
CHĀRACTERIZATION, FUNCTION, MYRISTOYLATION, PHOSPHORYLATION,
INTERACTION WITH ZAP70 AND CBL, AND MUTAGENESIS OF GLY-1; MET-26 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARG-119.
MEDLINE=22022020; PubMed=12024036;
LOTELO M.P., Berry D.M., McGlade C.J.;
LOTECT M.P., Berry D.M., McGlade C.J.;
LOTECTIONAL COOPERATION between c-Chl and Src-like adaptor protein in the negative regulation of T-cell receptor signaling.";
Mol. Cell. Biol. 22:4241-4255(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INITIATION,
                                                                                                                                                                                                                                                                                                                                                                                                      SLA2_MOUSE STANDARD; PRT; 258 AA.
QBR4L0; QBCOK2; QBV142; Q9D1Z9;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
SrC-lke-adapter 2 (SrC-like adapter protein-2) (SLAP-2).
SLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORMS 1 AND 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 277:19131-19138(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22013997; PubMed=11891219;
                                                                                                                                                                                                                                                                                                 RESLSFYISLNDEAVSLDDA 260
                                                                                                                                                                                                                                                         RESLSFYISLNDEAVSLDDA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                           61
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SLA2 MOUSE
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PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
Immune response; Membrane; SH2 domain; SH3 domain; Myristate; Phosphorylation; Alternative initiation; Lipoprotein.
INIT WET 1 25R

HERBY, POG229; LLKT.

MGD; MG1:1925049; Sla2.

MGD; GO:0016023; C:cytcoplasmic vesicle; IDA.

GO; GO:0005770; C:late endosome; IDA.

GO; GO:000586; C:plasma membrane; IDA.

GO; GO:0005110; F:procein binding; IDA.

GO; GO:0004110; P:T-cell activation; IDA.

InterPro; IPR000960; SH2.

InterPro; IPR001452; SH3.

Pfam; PF00017; SH2:1.

PRINTS; PR00401; SH2:1.

PRODGM: PR00093; SH2:1.

SMART; SM03252; SH3:1.

EMBL, AF287467; AAL38196.1; EMBL, AF434990; AAL86403.1; EMBL, AKO20837; BAB32223.1; ALT_INIT. EMBL, AKO30877; BAC27168.1; EMBL, AKO308672; BAC40495.1; -..

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                                                                                                                                                                                                                                                                                                                                                                                                                       Event-Alternative initiation,
Comment-2 isoforms, 1/p28 (shown here) and 2/p25, are produced
by alternative initiation at Met-0 and Met-26;
TISSUE SPECIFICITY: Mainly expressed in immune system. Highly
expressed in sphen and thymus and expressed at intermediate
levels in lung. Not expressed in liver, heart and brain. Isoform is predominant in lung and spleen, while isoform 2 is predominant
                                                                                                                                                                                      receptor (TCR) signaling. Inhibits T-cell antigen-receptor induced activation of nuclear factor of activated T-cells. May act by linking signaling proteins such as ZAP70 with CBL, leading to a CBL dependent degradation of signaling proteins.

-!- SUBUNIT: Interacts with phosphorylated CBL via its C-terminal domain. Interacts with phosphorylated proteins ZAP70 and CD3Z via
                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuan Z., Zavolan M., Zhu Y., Zinmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S., Hara A., Hashizume W., Indiawa K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Marasinishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Sasaki W., Sasaki Y., Shibata K., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Materston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Waterston R., Lander E.S., Rogers J., Mature 420:563:573 (2002).
                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic; localized to the plasma membrane and intracellular vesicles, including late endosomal
                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                              its SH2 domain.
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Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                              Similarity
 similarity)
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                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                              182 DICCLIKEPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEA-ATGEBSLLSEG 240
                                                                                                                                                                                                                     59
                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity). SUBJUT: Homodimer. Interacts with phosphorylated CBL, SYK and ENGUNIT: Homodimerization and interaction with phosphorylated CBL occurs via its C-terminal domain. Interacts with prosphorylated proteins ZAP70; CD3Z; VAVI and EPH24 its SH2 domain (By similarity). SUBCELLUIAR LOCATION: Cytoplasmic; colocalizes with endosomes (By
                                                                                                                                                                                                                                                  120 ESQTRRGCYSLSVRLSRPASWDRIRHYRIQRLDNGWLYISPRLTFPSLHALVEHYSELAD
                                                                                                                                                                                                                                                                                                                         ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSBLAD
                                                                                                                                                                                                    2 GSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTI
                                                                                                                                                                                                                    GSLSSRGKT-SSPSSSGPDQEPVSMQPERHKVTAVALGSFPAGEQARLSLRLGEPLTI
                                                                                                                                                                                                                                        VSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIR
                                                                                                                                                                                   Gaps
                                                                                                R->E: ABOLISHES INTERACTION WITH ZAP70,
AND ITS INHIBITORY FUNCTION.
                                                                 M->V: ABOLISHES ISOFORM 2.
P->L: DOES NOT AFFECT ITS INHIBITORY
FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rai
NCBI_TaxID=10116;
                                                                                                                                                                                   4,
                                                                                                                                                                Score 1023; DB 1; Length 258;
Pred. No. 1.8e-78;
                                     SLA C-TERMINAL.
N-myristoyl glycine.
G->A: ABOLISHES LOCALIZATION
                                                                                                          AND ITS INHIBITORY FUNCTION.
C -> Y (IN REF. 3; BAC27168).
S -> T (IN REF. 2).
F -> H (IN REF. 2).
8270E93DE3FC696A CRC64;
SRC-LIKE-ADAPTER 2, ISOFORM FOR ISOFORM 2.
                                                                                                                                                                                   34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SRC-like-adapter (Src-like-adapter protein 1)
SLA OR SLAP OR SLAP1.
Rattus norvegicus (Rat)
                                                                                                                                                          75.6%; Scor. 79.3%; Pred. No. 1... 79.3%; Pred. Nismatches
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                                                                MEMBRANES
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LRESLSSYISLAED--PLDDA 258
                                                                                                                                                28345 MW;
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160
258 AA;
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Best Local Similarity
Matches 207; Conserv
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P59622;
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CONFLICT
CONFLICT
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          INIT MET
DOMAIN
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DOMAIN
LIPID
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 LADDICCLLKEPCVLQR----AGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LPGPSTSRGEKEMGNSMKSTPAPLERPLSNTEGLESDFLAVLNDYPSPDISPPIFRGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LESPSISSSVQGQG-----PVTMEAERSKATAV-----ALGSFPAGGPAELSLRLGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Gaps
DOWAIN: The C-terminal domain is essential for the homodimerization and the interaction with CBL. While the homodimerization and the interaction with CBL is apparently mediated via the hydrophobic region of this domain, the highly charged region is apparently required for the homodimerization (By similarity).

FYM: Phosphorylated (By similarity).

SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 312 SLA C-TERMINAL.
312 AA; 34744 MW; A05412D39AE68388 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (mSLAP)
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41.3%; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIA1_MOUSE STANDARD; PRT; 280 AA.

AC 060858 Q8CQ96; Q8CATO; Q8CBE9; Q8QZX8;

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT SRC-like-adapter (Src-like-adapter protein 1)

GN SIAP OR SIAP1.

OS MUS musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EESLISEGLRESISFYISL-NDEAVSLD 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 LRVDESLFSYGLRESIASYLSLTGDDSSNFD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH2 domain; SH3 domain; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY217759; AAO61134.1; -.
InterPro; IPR001980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRODOM; PD000093; SH2; 1.
SMART; SM00326; SH2; 1.
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8
P SEQUENCE: FROW N.A. (ISOCHES) I AND 2).

ANDLINE=22354683; PubMed=12466851;
A OKAZAKI Y., FURTUO M., KASUKAWA T., Adachi J., Bono H., Kondo S.,
ANDLINE=22354683; PubMed=12466851;
A NEDLINE=22354683; PubMed=12466851;
A Nikaido I., Sauton M., Kasukawa T., Adachi H., Yamanaka I., Kiyosawa H.,
A Nikaido I., Sauton M., Saiton R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Nadiari I.M., Kanapin A., Matsuda H., Schonbach C., Gojobori T.,
A Bake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
A Schriml I.M., Kanapin A., Matsuda H., Crerest A., Frazer K.S.,
A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
A Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
A Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenbard B.L., Marchionni L., Machorie L., Mit H.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenbard B., Lyons P.A.,
A Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
BA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
A Sultana R., Takenaka Y., Taylor M.S., Tasmachandran S.,
A Varanco R., Wagner L., Wahleetett C., Wang Y., Watanabe Y., Walls C.,
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A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sasaxi A.,
A Sasaxi A., Sasaxi K., Sasaxi D., Shinagawa A.,
A Hashaya K., Hashizume W., Imctail M., Sasaxi D., Shinagawa A.,
A Harney E., Hayashizaki X.,
B Harney E., Hayashizaki X.,
B Harney E., Hayashizaki X.,
B Harney E., Hayashizaki X.,
B Harney E., Hayashizaki X.,
B Harney E., Hayashizaki X.,
B Harney E., Shinaga Banotalon G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-2388257; PubMed=1247932;
MEDINE-2388257; PubMed=1247932;
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                 TISSUE=Embryonic brain,
MEDLINE=95370243; PubMed=7543898;
Pandey A., Duan H., Dixit V.M.
Characterization of a novel Src-like adapter protein that associates with the Eck receptor tyrosine kinase.";
J. Biol. Chem. 270:19201-19204(1995).
[1]
SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ILS, and ISS;
MEDLINE=21363810; PubMed=11471062;
MEDLINE=21363810; PubMed=11471062;
MEDLINE=71363810; PubMed=11471062;
MEDLINE=71363810; PubMed=11471062;
MEDLINE=21363810; PubMed=11471062;
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MEDLINE=21363810;
MEDLINE=21363810;
MEDLINE=21363810;
MEDLINE=2136381
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20093985; PubMed=10630289;
Garriar A., Mayven C., Victorero G., Granjeaud S., Rocha D.,
Bernard K., Miazek A., Ferrier P., Malissen M., Naquet P.,
Malissen B., Jordan B.R.;
"Differential gene expression in CD3epsilon- and RAG1-deficient
thymucses: definition of a set of genes potentially involved in
thymucyte maturation.";
Immunogenetics 50:255-270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 within alcohol-related OTLs.";
Mamm. Genome 12:657-663 (2001).
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MEDILINE-21453118; PubMed=1156785;
A SOSINOWAKI T., Killeen N., Weiss A.;
Sosinowaki T., Killeen N., Weiss A.;
Sosinowaki T., Killeen N., Weiss A.;
The Src-like adaptor protein down-regulates the T cell receptor on CD4+CD8+ thymocytes and regulates positive selection.";
Immunity 15:457-46(2001).
Immunity 15:457-46(2001).
Immunity 15:457-46(2001).
Immunity 15:457-46(2001).
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Inmunity 15:457-46(2001).
Inmunity 15:457-46(2001).
Inmunity 15:457-46(2001).
Inmunity 15:457-46(2001).
Inmunity 15:457-46(2001).
Induced activation of positive selection and mitcsis of T-cells.
May act by linking signaling proteins such as ZAP70 with CBL.
Induced activation of positive selection of signaling proteins.
Induced activation and interaction with phosphorylated CBL.
Int. Homodimerization and interaction with phosphorylated CBL.
Cocurs via its C-terminal domain (By similarity). Interacts with PDGFRB and BPHA2. Interacts with phosphorylated proteins ZAP70,
CD32; VAVI and LCP2 via its SH2 domain.
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoid=Q60898-2; Sequence=VSP_007239;
ISSUB SPECIFICITY: Predominantly expressed in lymphoid tissues.
Higly expressed in spleen, thymus and lymph nodes. Weakly
expressed in lung and brain. Expressed in I-cells and at low level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: Expressed during thymocyte maturation. Weakly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manes G., Bello P., Roche S.; "Stap negatively regulates Strong function but does not revert "Stap negatively regulates Strong Stable and Cell morphology changes."; Mol. Cell. Biol. 20:3396-3406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: The C-terminal domain is essential for the homodimerization and the interaction with CBL. While the interaction with CBL is apparently mediated via the hydrophobic region of this domain, the highly charged region is apparently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, SUBCELLULAR LOCALIZATION, MYRISTOYLATION, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCP2, AND MUTAGENESIS OF PRO-72 AND ARG-110.
MEDLINES-20130290; PubMed-10662792;
Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
"Src-like adaptor protein (SLAP) is a negative regulator of T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic; colocalizes with endosomes. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98414809, PubMed-9742401;
Roche S., Alonso G., Kazlauskas A., Dixit V.M., Courtneidge S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in CD4(-) CD8(-) thymocytes, strongly expressed in CD4(+) CD8(+) thymocytes, while expression decreases in more mature cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, INTERACTION WITH ZAP70; CD3Z; VAV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pandey A.;
"Src-like adaptor protein (Slap) is a negative regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q60898-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF GLY-1.
MEDLINE=20242033; Pubmed=10779329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 191:463-474(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH PDGFRB.
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Miura Y.;
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 KKGFYSLSVR-----HRQVKHYRIFRLPNNWYYISPRLTFQCLEDLVTHYSBVADGLCC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LLKEPCVLQR-----AGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSBAATG----BESL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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required for the homodimerization (By similarity).

PTM: Phosphorylated (By similarity).

MISCELLANEOUS: SLA deficient mice show a strong upregulation of TCR and CDS at the CD4(+) CD8(+) stage, and an enhanced positive selection in T-cells.

SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 280;
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PROSITE; PS50001; SH2; 1.
SH2 domain; SH3 domain; Myristate; Phosphorylation; Alternative splicing; Lipoprotein.
INIT MET 21 81 SH3.
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SH2.
SLA C-TERMINAL.
N-myristoyl glycine.
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43.6%; Pred. No. 6.2e-34;
tive 38; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 LSEGLRESLSFYISL-NDEAVSLD 259
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                                                                                                                                                                                                                                                                                                  AY079450; AAL87538.1; -... AK036167; BAC2928.1; -... AK03401; BAC29896.1; -... AK041265; AAH32922.1; -...
                                                                                                                                                                                                                                                                    AJ13177; CAB66139.1; -. AY079449; AAL87537.1; -.
                                                                                                                                                                                                                                                                                                                                             EMBL; AKC41565; BAC30988.1; -
BMBL; BC032922; AAH32922.1; -
BMSP; P16277; 1BLK.
MGD; MGI:104295; Sla.
InterPro; IPR001980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                        U29056; AAA82756.1; -.
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Best Local Similarity 43.6%
Matches 115, Conservative
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275 AA.

PRT;

STANDARD;

RESULT 5 SLA1_HUMAN ID SLA1_HUMAN ST AC Q13239; Q9UMQ8;

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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=96423064; PubMed=8825655; A., Pandey A.; Angrist M., Wells D.E., Chakravarti A., Pandey A.; Angrist M., Wells D.E., Chakravarti A., Pandey A.; Chromosomal localization of the mouse Src-like adapter protein (Slap) gene and its putative human homolog SLA."; Genomics 30:623-625(1995).
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Biochem. Biophys. Res. Commun. 230:81-84(1997).
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Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euterperia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Histiocytic lymphoma;
MEDLINE-97148576; PubMed-9020066;
Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
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MEDLINE=21100465; PubMed=11179692;
Kratchmarova I., Sosinowski T., Weiss A., Witter K., Vincenz C.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
SLG-like-adapter (Src-like-adapter protein 1) (hSLAP).
SLA OR SLAP OR SLAPI.
Homo sapiens (Human)
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24 723; LEU-223 AND LAT, AND MUTAGENESIS OF ARG-110; LEU-217;
25 LEU-223; LEU-228 AND 236-LEU-LEU-238.

26 LEU-223; LEU-229 AND 236-LEU-LEU-238.

27 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

28 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

29 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

20 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

21 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

22 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

23 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

24 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

25 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

26 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

27 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

28 Tang J., Sayasting S.J.,

29 Tang J., Sawasdikosol S., Chang J.-H., Burakoff S.J.;

20 Tang J., Sayasting S.J.,

20 Tang J., Sayasting S.J.,

21 Tang J., Sayasting S.J.,

22 Tang J., Sayasting S.J.,

23 Tang J., Sayasting S.J.,

24 Tang J., Sayasting S.J.,

25 Tang J., Sayasting S.J.,

26 Tang J., Sayasting S.J.,

27 Tang J., Sayasting S.J.,

28 Tang J., Sayasting S.J.,

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29 Tang J., Sayasting S.J.,

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20 Tang Poperhory S.J.,

20 Tang Poperhory S.J.,

21 Tang J., Sayasting S.J.,

22 Tang J., Sayasting S.J.,

23 Tang J., Sayasting S.J.,

24 Tang J., Sayasting S.J.,

25 Tang J., Sayasting S.J.,

26 Tang J., Sayasting S.J.,

27 Tang J., Sayasting S.J.,

28 Tang J., Sayasting S.J.,

28 Tang J., Sayasting S.J.,

29 Tang J., Sayasting S.J.,

20 Tang J., Sayasting S.J.,

20 Tang J., Sayasting S.J.,

21 Tang J., Sayasting S.J.,

22 Tang J., Sayasting S.J.,

23 Tang J., Sayasting S.J.,

24 Tang J., Sayasting S.J.,

25 Tang J., Sayasting S.J.,

26 Tang J., Sayasting S.J.,

27 Tang J., Sayasting S.J.,

28 Tang J., Sayasting S.J.,

29 Tang J., Sayasting S.J.,

20 Tang J., Sayasting S.J.,

20 Tang J., Sayasting 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMB outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Expressed in lung and fetal brain. Weakly verpressed in heart, adult brain, placenta, liver, skeletal muscle, kidney and pancreas.

INDUCTION: By all-trans retinoic acid (ATRA). Induction is indirect and is mediated through other proteins.

DOMAIN: The C-terminal domain is essential for the homodimerization and the interaction and the interaction and the interaction with CBL is apparently mediated via the hydrophobic region of this domain, the highly charged region is apparently required for the homodimerization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic; colocalizes with endosomes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH2.
SLA C-TERMINAL.
N-MYZISCOYl Glycine (By similarity).
R->K: STRONGLY REDUCES INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINCES PROOFIGE SHEET TO PROMAIN.

PRODOM; PROOFIGE SHEET I.

SWART; SMO0252; SH2; I.

SWART; SMO0252; SH3; I.

PROSITE; PS50001; SH3; I.

PROSITE; PS50001; SH3; I.

SH2 domain; SH3 domain; Myristate; Phosphorylation; Lipoprotein.

INIT_MET 0 0 BY SIMILARITY.

DOMAIN 83 174 SH2.
Pandey A.; "Characterization of promoter region and genomic structure of murine and human genes encoding Src like adapter protein."; Gene 262:267-273 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D89077; BAA13758.1; -.
EMBL; U44403; AAC27662.1; -.
EMBL; BC007042; AAH07042.1; -.
EMBL; AJ238591; CAB53536.1; -.
HSSP; P08631; 3HCK.
Genew; HGNC:10902; SLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U30473; AAC50357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPID
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 SYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 FYSLSVR-----HRQVKHYRIFRLENNWYYISPRLTFQCLEDLVNHYSEVADGLCCVLT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 KSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 WKAISLSTGRESYIPGICVARVYHGWLFBGLGRDKAEELLQLPDTKVGSFMIRESETKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 EPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG-----EESLLSEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87172710; PubMed=3561390;
Yamanashi Y., Fukushige S.-I., Semba K., Sukegawa J., Miyajima N.,
Matsubara K.-I., Yamamoto T., Toyoshima K.;
"The yes-related cellular gene lyn encodes a possible tyrosine kinase
similar to ps61ck.";
ZAP70, CD3Z, SYK AND LAT.

L-SS: ABOLIGHES INTERACTION WITH CBL,
WHILE IT DOES NOT AFFECT DIMERIZATION
WHEN ASSOCIATED WITH S-224 AND S-229.

L-SS: ABOLIGHES INTERACTION WITH CBL,
WHILE IT DOES NOT AFFECT DIMERIZATION
WHEN ASSOCIATED WITH S-218 AND S-229.

L-SS: ABOLIGHES INTERACTION WITH CBL,
WHILE IT DOES NOT AFFECT DIMERIZATION
WHEN ASSOCIATED WITH S-218 AND S-224.

LSL->OSQ: ABOLISHES INTERACTION WITH CBL
SLIGHTLY AFFECT DIMERIZATION
Y -> D (IN REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILNE=94171041; PubMed=8125304;
MEDILNE=94171041; PubMed=8125304;
MEDILNE=94171041; PubMed=8125304;
Mider L.G., Raben N., Miller L., Jelsema C.;
The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in rat mast cells and human myeloid cells.";
Gene 138:219-222(1994).

-:- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                         35.6%; Score 481.5; DB 1; Length 275; 40.3%; Pred. No. 4.1e-33; ive 43; Mismatches 85; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
Name=LYN A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Tyrosine-protein kinase LYN (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to p561ck.";
Mol. Cell. Biol. 7:237-243(1987).
                                                                                                                                                                                                                                                                                                                                                           31025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 RESLSFYISLNDE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||::|:|
229 RESIASYLSLTSE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
                                     217
                                                                                                                                                                                                228
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                                                                                                                223
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                                                                                                                                                                                                                                                                                                                              70
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                   228
                                                                                                                                                                                                                                                                           236
                                     217
                                                                                                             223
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P07948;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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66 GDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIR
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY).
Missing (in isoform LYN B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity) SH3.
                                                      IsoId=P07948-2; Sequence=VSP_005002;
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.4%; Score 370.5; DB 1; Length 511; 39.8%; Pred. No. 1.8e-23; ive 36; Mismatches 76; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frid=VSP 005002.
8419CD461204E364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0451, SH2DOMAIN.
PRINTS; PRO0452, SH3DOMAIN.
PRINTS; PRO0452, SH3DOMAIN.
PRINTS; PRO0109; TYKINASE.
ProDom; PD0000091; Proc. Kinase; 1.
ProDom; PD0000065; SH3; 1.
SWART; SW00252, SH3; 1.
SWART; SW00226; SH3; 1.
SWART; SW00219; TYRK; 1.
PROSITE; PS00109; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; SH3; 1.
        IsoId=P07948-1; Sequence=Displayed;
                                                                                                                                 -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 AA; 58442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M16038; AAA59540.1; -.
EMBL, M7321; AAB50019.1; -.
PIR; A26719; TVHULY.
HSSP, P08631; 1AD5.
Genew; HGNC:6735; LYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165120;
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MOD RES
MOD RES
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DOMAIN
NP BIND
BINDING
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SEQUENCE FROM N.A. (ISOFORM LYN A).

SIGNIBLE FROM N.A. (ISOFORM LYN A).

STRAIN-CZech II; TISSUE-Mammary gland;

XA Straiber R.L., Peinold E.A., Grouse L.H., Derge J.G.,

ALISCHIIS R.F., Zeeberg B. Buetow K.H., Schweier C.M., Schuler G.D.,

Alischil S.F., Zeeberg B. Buetow K.H., Schweier C.P., Bhat N.K.,

Alischil S.F., Zeeberg B. Buetow K.H., Schweier C.P., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldon M.F., Carannor T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonshiyuki S., Carannor P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.M.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.M.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.M.,

A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rader G.C., Grimwood J., Schmutz J., Myers R.M.,

R Rodriguez A.C., Grimwood J., Schmutz J., Nevsen M.C.,

R Schnerch A., Schein J.B., Jones S.J.W., Marra M.A.,

R Schnerch A., Schein J.B., Jones S.J.W., Marra M.A.,

R Hunan and mouse cDNA sequences.

R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                    96 GEWWKAKSLLIKKEGFIPSNYVAKLNTLETEEWFFKDITRKDAERQLLAPGNSAGAFLIR
                                                            122 ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 363-431 FROM N.A.
MEDIATE-90152381, PubMed-248288;
MEDIATE-90152381, PubMed-248288;
Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
"The application of the polymerase chain reaction to cloning members of the protein tyrosine kinase family.";
Gene 85:67-74(1989).

-- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91260688; PubMed=1710766; Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A., Lock P., Dunn A.R., "Alternatively spliced murine lyn mRNAs encode distinct proteins."; Mol. Cell. Biol. 11:3399-3406(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91203857; PubMed=2017160;
Yi T., Bolen J.B., Ihle J.N.;
"Hematopoietic cells express two forms of lyn kinase differing by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
Tyrosine-protein kinase LYN (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids in the amino terminus."; Mol. Cell. Biol. 11:2391-2398(1991).
                                                                                                                                                     182 DICCLLKEPCVLQRAGPLPGK 202
                                                                                                                                                                                  :| |:: |:
216 GLCRRLEKACI----SPKPQK 232
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                LYN MOUSE
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| :: | | : | | : | | : | | : | | SNKQQRPVPE-SQLLPGQRFQTKDPEBEQGDIVVALYPYDGIHPDDLSFKKGERWKVLEEH 95

37

6 SRRKSLPSPSLSSSVQGQGPVTWEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED

80; Conservative

Best Local Similarity Matches 80; Conserv

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511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=LYN A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=LYN B;
431
                             Query Match
Best Local S:
Matches 81
                                                                                                                                                       122
CONFLICT
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                                                                                                                                                                                                                                                                      LYN RAT
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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the FNBL cutstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
Missing (in isoform LYN B).
                                                  IsoId=P25911-2; Sequence=VSP 005003;
TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and
                                                                                 SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-myristoyl glycine (By similarity). S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
Transferase, ATP-binding; Myristate; SH2 domain; SH3 domain;
Palmitate; Lipoprotein; Alternative splicing:

INIT MET

1 N-myristoyl qlycine (By similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
         Event=Alternative splicing, Named isoforms=2;
Name=LYN A;
IsoId=P25911-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN REF.
(IN REF.
(IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM02125; SH2; 1.
SMART; SM02125; SH3; 1.
SMART; SM02126; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                EMBL, M64608; AAA39470.1;
EMBL, M57696; AAA39471.1;
EMBL, M57697; AAA39471.1;
EMBL, M57697; AAA39471.1;
EMBL, M3426; AAA40017.1;
PIR, A39719; A39719.
HSSP, P08631; 1AD5.
HSP, P08631; 1AD5.
INCEPPO: IPRO00790; SH3.
INCEPPO: IPR000790; SH3.
INCEPPO: IPR000145; SH3.
INCEPPO: IPR000455; SH3.
INCEPPO: IPR000455; SH3.
INCEPPO: IPR000455; PYP. PKINASE.
INCEPPO: IPR000455; PYP. PKINASE.
INCEPPO: IPR000455; PYP. PKINASE.
INCEPPO: IPR000455; PXINASE.
INCEPPO: IPR000456; PXINASE.
INCEPPO: IPR00045; PXINASE.
INCEPPO: IPR00045; SH3.
PÉAM; PF000017; SH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VSP
                                                                                                   SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 1 SH3 domain.
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PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
ProDom; PD0000093; SH2; 1.
ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76
160
278
390
414
424
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2225
2225
224
224
366
507
44
                                                                       myeloid cells
                                          Name=LYN B;
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CONFLICT
CONFLICT
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DOMAIN
NP BIND
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215
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                                                                                                                                                                                                                                                                        | :: | | : | | : | | : | | : | | SNKQQRPVPEF-HLLPGQRFQTXDPEEQGDIVVALYPYDGIHPDDLSFKKGEKMKVLEEH 95
                                                                                                                                                                                                                                 6 SRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (2) SEQUENCE FROM N.A.
MEDIJINE=94171041; Pubmed=8125304;
Rider L.G., Raben N., Miller L., Jelsema C.;
The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in rat mast cells and human myeloid cells.";
Gene 138:219-222(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Minoguchi K., Nishikata H., Siraganian R.P.;
Minoguchi K., Nishikata H., Siraganian R.P.;
"Bacterially expressed rat p561yn binds several proteins in rat
basophilic leukemia cells including pp72, a tyrosine phosphorylated
Drotein prominent in activated cells.";
J. Immunol. 150:222-222(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-9744244; PubMed=9295361;
MEDLINE-9744244; PubMed=9295361;
Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
Vonakis B.M., chen H., Haleem-Smith H., Metzger H.;
The unique domain as the site on Lyn kinase for its constitutive association with the high affinity receptor for IgE.";
J. Biol. Chem. 272:24072-24080(1997).
-:- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=007014-2; Sequence=VSP 005004;
-!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and myeloid cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                                                                                                                 6
                                                                                             DB 1; Length 511;
                                                                                         ch 27.2%; Score 367.5; DB 1; Length I Similarity 40.3%; Pred. No. 3.2e-23; 81; Conservative 33; Mismatches 78; Indels
L -> P (IN REF. 4).
3935221CC90C50F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     007014; Q63320;
01-UN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase LYN (BC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 DICCLLKEPCVLQRAGPLPGK 202
                                58681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 GDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 GEWWXAKSLSSKREGFIPSNYVAKVNTLETEEWFFKDITRKDAERQLLAPGNSAGAFLIR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESQIRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLIFPSLQALVDHYSELAD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 SRRKSLPSPSLSSSVQGQGPVTWEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 SNKQQRPVPE-SQLLPGQRFQAKDPEBQGDIVVALYPYDGIHPDDLSFKKGEKMKVLEBH 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

MISSING (In isoform LYN B).

/ FITG=VSP 005004.

P -> L (IN REF. 2).

V -> A (IN REF. 2).

C -> Y (IN REF. 2).

C -> Y (IN REF. 2).

WW, 24AZESEZ29CD43ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-myristoyl glycine (By similarity).
S-palmitoyl cysteine (By similarity)
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.2%; Score 367.5; DB 1; Length 511; 40.3%; Pred. No. 3.2e-23; tive 33; Mismatches 78; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
Transferase; Lipoprotein; Alternative splicing.
INIT MET 1 1 N-myristoyl glycine (By similar: LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SM00252; SH2; 1.
SWART; SM00252; SH2; 1.
SWART; SM00219; TyrCc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                     InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Flam; PF000069; pkinase; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DWAIN.
PRINTS; PR00402; SH3DOWAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000001; Prot_kinase; 1.
ProDom; PD0000001; Prot_kinase; 1.
ProDom; PD0000066; SH3; 1.
                                                                                                                                                                                                                                                         InterPro; IPR000719; Prot_kinase.
InterPro; IPR000980; SH2.
                                                                                                                                                                         EMBL; AF000300; AAB71344.1; -... EMBL; AF000301; AAB71345.1; -... EMBL; AF000302; AAB71346.1; -... PIR; IS6160; IS6160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58529 MW;
                                                                                                                            EMBL; L14951; AAA41549.1; -. EMBL; L14782; AAA20944.1; -. EMBL; L14823; AAA20945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.2%
Best Local Similarity 40.3%
Matches 81; Conservative
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225
236
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BINDING
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MOD RES
MOD RES
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SEQUENCE
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TISSUES-Cell,

MEDLINE=2288257, PubMed=12477932,

MEDLINE=2288257, PubMed=12477932,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altschul S.F., Jordan H., Moore T. Mang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B.K., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodersation and initial analysis of more than 15,000 full-length
215
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TISSUB=11eal mucosa;

Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,

Kawakami T., Noguchi S., Itoh T., Shigeta M., Tanigami A., Fujiwara T., Ono T.,

Vamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T.,

Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,

Isogai T., Sugano S.,

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87257943; PubMed=3453117; Ziegler S.F., Marth J.D., Lewis D.B., Perlmutter R.M.; Marth J.D., Lewis D.B., Perlmutter R.M.; Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of hematopoletic origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21-525 FROM N.A. MEDIATE 317-57942; BubMedia3496523; MEDIATE-8757942; BubMedia3496523; Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J., Lebo R., Varmus H., Bishop J.M., Pettenati N.J. Lebo R., Varmus H., Diaz M.O., Rowley J.D.; that encodes a protein-tyrosine "Indentification of a human gene (HCK) that encodes a protein-tyrosine kinase and its expressed in hemopolatic cells."; Mol. Cell. Biol. 7:2267-2275(1987).
156 ESETLKGSFSLSVRDYDPMHGDVIKHYKIRSLDNGGYYISPRITFPCISDMIKHYQKQSD
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                           HCK HUMAN STANDARD; PRT; 525 AA.
P08531; Q96CC0; Q9H5Y5; Q9NUA4; Q9UMJ5;
01-AUG-1988 (Rel. 08, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK/p60-HCK)
(Hemopoietic cell kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells of hematopoietic origin.";
Mol. Cell. Biol. 7:2276-2285(1987).
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MEDLINE=21638749; PubMed=11780052;
                                                   182 DICCLLKEPCVLQRAGPLPGK 202
                                                                                               216 GLCRRLEKACI----SPKPOK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 21-525 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-525 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Deloukas P., Matthews D.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Balley V., Barlow K.F., Bares K.N., Barden D.M., Berare D.M.
Beasley O.P., Bird C.P., Blakes K.S., Bridgeman A.M., Brown A.J.,
Beasley O.P., Bird C.P., Blakes Y.S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dunn M.,
Blington A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Blington A.G., Frankland J.A., Fraser A., French L., Garmer P.,
Altarham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Anckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Ray M.P., Kimberley A.M., King A., Kriights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachle L.J., McLay R., McMurray A.R.,
Milne S.A., Mistry D., McConnachle L.J., McLay K., McMurray A.R.,
Allilmore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
Aracey A., Tromans A.C., Vaudin M., Wallis J.W.,
Hhitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Hilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Hallming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Halley B. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Halley B. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Halley D. W. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Halley D. W. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Halley D. W., Beck M. T., Beck M. T.,
Halley D. W., Welley M., Bentley D.R., Welley Beck S.,
Halley D. W., Welley M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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MEDLINE-98239731; PubMed=9571048;
HOTICA D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
Gmeiner W.H., Byrd R.A.;
"Solution structure of the human Hck SH3 domain and identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-21 FROM N.A., AND ALTERNATIVE INITIATION.
MEDLINE=91342636; PubMed=1875927;
Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
"Two isoforms of murine hck, generated by utilization of alternative translational initiation codons, exhibit different patterns of subcellular localization.";
Mol. Cell. Biol. 11:4363-4370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97263497; PubMed=9109402; Zhang W., Smithgall T.E., Gmeiner W.H.; Zhang W., Smithgall T.E., Gmeiner W.H.; scruptential assignment and secondary structure determination for the Src homology 2 domain of hematopoietic cellular kinase."; FEBS Lett. 406:131-135(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hradetzky D., Strebhardt K., Ruesamen-Waigmann H.;
"The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of exon-intron structure among human PTKs of the scr family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "RT loop flexibility enhances the specificity of Src family SH3 domains for HIV-1 Nef.";
Blochemistry 37:14683-14691(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 80-136.
MEDLINE=88453315; PubMed=9778343;
Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
Ladbury J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sicheri F., Moturefi I., Kuriyan J.;
"Crystai structure of the Src family tyrosine kinase Hck.";
Nature 385:602-609(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Spleen;
MEDLINE=92241680; PubMed=1572549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4EDLINE=97177106; PubMed=9024658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       its ligand binding site.";
J. Mol. Biol. 278:253-265(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 178-525 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 138-244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 113:275-280(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White.
Wilming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA
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   FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 PSPSLSSSVQGQGPVIMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 LSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRR
                                                                                                                                                                                                                                            (By
                                                                                                                                                                                                        SÜBCELLULÄR LÖCATION: Isoform p60-HCK and isoform p59-HCK are associated with membranes, Isoform p60-HCK is also cytoplasmic
                                                                                                                                                                                                                                                                         similarity).
ALTERNATIVE PRODUCTS:
Event-Alternative initiation;
Comment=2 isoforms, p60-HCK (shown here) and p59-HCK, are
produced by alternative initiation;
TISSUE SPECIFICITY: Expressed predominantly in cells of the
myeloid and b-lymphoid lineages.
SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
FUNCTION: May serve as part of a signaling pathway coupling th receptor to the activation of the respiratory burst. May also contribute to neutrophil migration and may regulate the degranulation process of neutrophils.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R PDB; 5HCK; 17-UXN-29.

R PDB; 1AD5; 15-MAY-97.

R PDB; 1BU1; 11-UXN-98.

R PDB; 1BU1; 11-UXN-98.

R PDB; 1GCF; 08-UXN-99.

R MIM; 142370; 08-UXN-99.

R MIM; 142370; 18-DECT HORGINE Kinase activity; TAS.

GO; GO:0004413; F:protein-tyrosine kinase activity; TAS.

GO; GO:0004413; F:protein-mino acid phosphorylation; TAS.

GO; GO:0004413; P:protein mino acid phosphorylation; TAS.

R GO; GO:0006468; P:protein mino acid phosphorylation; TAS.

R O:0006468; P:protein mino acid phosphorylation; TAS.

R InterPro; IPR00199; Prot. Kinase.

R InterPro; IPR00155; TYY pkinase.

R InterPro; IPR00156; TYY pkinase.

R Pfam; PF00017; SH2; 1.

R Pfam; PF00017; SH2; 1.

R Pfam; PF00017; SH2; 1.
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26.6%; Score 360.5; DB 1
Best Local Similarity 41.6%; Pred. No. 1.3e-22;
Matches 77; Conservative 31; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X58741; CAA41565.2; -.
X58742; CAA41565.2; JOINED.
X58743; CAA41565.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC014435; AAH14435.1; -. AK026432; BAB15482.1; -. AL049539; CAB75606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M16591; AAA52643.1; -.
EMBL; M16592; AAA52644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                              tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; ZHCK; 20-AUG-97.
PDB; 3HCK; 15-OCT-97.
PDB; 4HCK; 17-JUN-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A27811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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117 RSLATRKEGYIPSNYVARVDSLETEEWFFKGISRKDAERQLIAPGNMLGSFMIRDSETTK 176
                                                  128 GSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLL 187
                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase HCK (BC 2.7.1.112) (p56-HCK) (Hemopoietic cell
                                                                                                                                                                                                                                                                                                                                                    Thesis (2001), University of Marseille, France.

-!- FUNCTION: May serve as part of a signaling pathway coupling the left receptor to the activation of the respiratory burst. May also contribute to neutrophil migration and may regulate the degranulation process of neutrophils (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

    -!- SUBCELLULĀR LOCATION: Membrane-associated (By similarity).
    -!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC

                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Bukaryots, Mereazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopitheciae; Macaca.
                                                                                                                                                                      503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfamily.SIMILARITY: Contains 1 SH2 domain.SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00252; SH2; 1.
SMART; SM00226; SH3; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS50011; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Prot_kinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001445; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PR00017; SH3: 1.
Pfam; PF00017; SH3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00401; SH2DDMAIN.
PR00452; SH3DDMAIN.
PR00109; TYRKINASE.
; PD0000001; Prot_kinase; 1.
; PD0000093; SH2; 1.
                                                                                                                                                                      PRT;
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                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
                                                                                                           237 SVPCM 241
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                   188 KEPCV 192
                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9541;
                                                                                                                                                                      HCK MACFA
                                                                                                                                                                                                                                           kinase).
HCK.
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Ргодом;
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PRINTS;
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Use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 WLYEGLSREKARELLILLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 VALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKV----SHG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and chromosomal localization of the human homologue of a B-lymphocyte specific protein tyrosine kinase (blk)."; Oncogene 10:477-486(1995).
-!- FUNCTION: May function in a signal transduction pathway that is restricted to B lymphoid cells.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-95123078; PubMed=7822795; Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.; Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.; Moblecular cloning, characterization, and chromosomal localization of a human lymphoid tyrosine Kinase related to murine Blk."; J. Immunol. 154:1265-1272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                            N-myristoyl glycine (By similarity).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
tyrosine phosphate.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLK HUMAN STANDARD; PRT; 504 AA.
P51451; Q16291;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 34, Last annotation update)
Tyrosine-protein kinase BLK (BC 2.7.1.112) (B lymphocyte kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                             1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95148218; PubMed=7845672;
Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
Niederhuber J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNGGFYISPRSTFSTLQELVDHYKKGSDGLCQKLSVPCV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 DNGWLYISPRLTFPSLOALVDHYSELADDICCLLKEPCV 192
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
26.5%; Score 358; DB 1,
Best Local Similarity 45.3%; Pred. No. 2e-22;
Matches 72; Conservative 29; Mismatches 5
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-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
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Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK/p59-HCK) (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).
                                                                   musculus (Mouse)
                                                                                                                                     NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
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    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 PPDEHLDEDKHFVVALYDYTAMNDRDLOMLKGEKLQVLKGTGDWWLARSLVTGREGYVPS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 VHVGKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 PVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPS 84
                                                                               EMBL; 233999; CAAB3965.1; --

EMBL; 276617; AAB33265.1; --

EMBL; 276617; AAB33265.1; --

EMBL; 376617; AAB33265.1; --

EMBL; 376617; BLK.

Genew; HGN:1057; BLK.

MIN; 191305; BLK.

MIN; 191305; Brotein kinase cascade; TAS.

GO: GO:0004713; F: protein kinase cascade; TAS.

MIN; 191305; Protein kinase.

EMETPEO: IPRO0019; Prote kinase.

INTERPEO: IPRO0145; SH3.

INTERPEO: IPRO0145; TYL_DKinase AS.

EMBL; PRO0169; PKINASE; I.

Pfam; PRO0169; PKINASE; I.

Pfam; PRO0109; PKINASE AS.

PRINTS; PRO0109; TYRKINASE.

PRODOM; PRO000001; PROTEIN KINASE TRR; FALSE_NEG.

PROSITE; PSO0117; PROTEIN KINASE TRR; FALSE_NEG.

PROSITE; PSO0117; PROTEIN KINASE TRR; FALSE_NEG.

PROSITE; PSO0117; PROTEIN KINASE TRR; FALSE_NEG.

PROSITE; PSO00127; PROTEIN KINASE DOM; I.

PROSITE; PSO00127; PROTEIN KINASE DOM; I.

PROSITE; PSO00127; PROTEIN KINASE DOM; I.

PROSITE; PSO00127; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

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PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

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PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

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PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

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PROSITE; PSO00137; PROTEIN KINASE DOM; I.

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PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROSITE; PSO00137; PROTEIN KINASE DOM; I.

PROTEIN DOM; PROTEIN KINASE DOM; I.

PROTEIN DOM; PROTEIN KINASE DOM; I.

PROTEIN DO
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SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
PROSPHORYLATION (AUTO-) (BY SIMILARITY).
M -> V (IN REF. 2).
I -> Y (IN REF. 2).
I -> Y (IN REF. 2).
Mw, BDBIDF50EC7370C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SWDRIRHYRIHCLDNGWLYISPRLTFPSLOALVDHYSELADDICCLLKEPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.1%; Score 352.5; DB 1; Length 504; Best Local Similarity 43.6%; Pred. No. 5.7e-22; Matches 75; Conservative 24; Mismatches 68; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 08, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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123
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HCK MOUSE
ID HCK MOUSE
AC PO8I03;
DT 01-AUG-1988
DT 10-OCT-2003
DT 10-OCT-2003
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NP BIND
BINDING
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                                                                                                                                                                                                                                   MEDIINE-88068587; PubMed=3317404;
Holtzman D.A., Cook W.D., Dunn A.R.;
"Isolation and sequence of a CDNA corresponding to a src-related gene expressed in murine hemopietic cells.";
Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Isoform p59-HCK and isoform p56-HCK are associated with membranes. Isoform p59-HCK is also cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- ALTERNATIVE PRODUCTS:

Bvent=Alternative initiation;

Comment=2 isoforms, p59-HCK (shown here) and p56-HCK, are produced by alternative initiation;
-!- TISSUE SPECIFICITY: Expressed predominantly in cells of the myeloid and b-lymphoid lineages.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                 Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                            SEQUENCE OF 21-523 FROM N.A.
STRAIN=ICR; TISSUE=Macrophage;
MEDLINE=88067781; PubMed=3684607;
Klemsz N.J., WarKercher S.R., Maki R.A.;
Nucleotide sequence of the mouse hok gene.";
Nucleotide Reg. 15:9600-9600(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIRE, A27282, TWMSHC.
HSSP, P08631, 1AD5.
MGD; MGI:96052, HCK.
INCEPPO: IPR000109; Neu cyt_fact_2.
INCEPPO: IPR000109; NEL kinase.
INCEPPO: IPR000199; NEL kinase.
INCEPPO: IPR001452; SH3.
INCEPPO: IPR001455; Tyr_pkinase.
INCEPPO: IPR001455; Tyr_pkinase.
Fam; PF00069; pkinase; 1.
Pfam; PF00019; SH3: 1.
Pfam; PF00011; SH3: 1.
Pfam; PF00019; SH3: 1.
PFINTS; PR00499; P67PHOX.
PRINTS; PR00499; P67PHOX.
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PROSITE; PS50001;
PROSITE; PS50002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                             S-palmitoyl cysteine (in isoform P56-HCK) (By similarity). PHOSPHORYLATION (AUTO-) (BY SIMILARITY). DF72FD726D89CE06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 DWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
TYROSINE-PROTEIN KINASE HCK, ISOFORM P59-
                                                                                                                                                                                                                                        TYROSINE-PROTEIN KINASE HCK, ISOFORM P56-
                                                                                                                                                                                                                                                                                                                                                            N-myristoyl glycine (By similarity).
N-myristoyl glycine (in isoform P56-HCK)
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LPSPSLSSSVQGQGPVTME---AERSKAT-AVALGSFPAGGPAELSLRLGEPLTIVSEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels 12; Gaps
                                                                                                                                                        Transferame; Tyrosine-protein kinase; Phosphorylation; ATP-binding; Lipoprotein; Myristate; Palmitate; SH2 domain; SH3 domain; Lipoprotein; Myristation.

BY SIMILABITY.

TYROSINE-PROTEIN KINASE HCK, ISOFORM PP.

CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.0%; Score 352; DB 1; Length 523; Best Local Similarity 41.0%; Pred. No. 6.6e-22; Matches 82; Conservative 33; Mismatches 73; Indels ...
                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                   FOR ISOFORM P56-HCK
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proc_kinase; 1.
ProDom; PD000006; SH3; 1.
SMART; SM00252; SH2; 1.
SWART; SM00326; SH3; 1.
SWART; SM00319; TYFKC; 1.
PROSITE; PS00109; PROFIEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00101; PROFIEIN KINASE DOM; 1.
PROSITE; PS00010; SH2; 1.
PROSITE; PS00001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                              408 PI
58998 MW;
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238
238
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378
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P50545; Q64647;
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SEQUENCE
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HDC RAT
HDC RD 554
AC P5054
DT 01-00
DT 10-00
DE TYCOS
DE TYCOS
DE RATU
OC BUKAX
OC BUKAX
OC BUKAX
OC NOB1
RN 6[1]
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RN 8[1]
RN 8[1]
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katius norvegitus (kat). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

Rattus norvegicus (Rat)

kinase).

NCBI_TaxID=10116;

SEQUENCE FROM N.A. MEDLINE=92109719; PubMed=1764064;

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Myrietate; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
Myrietate; Tyrosine-protein; SH3 domain; Lipoprotein.

T NIT MET; 0 0 1 8 Milharity.

T DOMAIN 120 217 8H3.

T DOMAIN 238 491 PROTEIN KINASE.

T DOMAIN 238 491 PROTEIN KINASE.

T NP BINDING 266 366 ATP (BY SIMILARITY).

T ACT SITE 357 357 BY SIMILARITY.

T LIPID 1 NPWISTCOY! Glycine (By Similarity).

T LIPID 1 NPWISTCOY! Glycine (By Similarity).

T CONFILCT 50 50 F - V (IN REF. 2).

T CONFILCT 204 26 K -> R (IN REF. 2).

T CONFILCT 305 305 M; 4CFCIF3FOESZEADF CRC64;
                                                                                                                                       Okano Y., Sugimoto Y., Fukuoka M., Matsui A., Nagata K.I., Nozawa Y.; "Identification of rat cDNA encoding hck tyrosine kinase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-myristcyl glycine (By similarity).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
F -> V (IN REF. 2).
F -> R (IN REF. 2).
I -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Membrane-associated.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                  megakaryocytes.";
Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00401; SH2DOWAIN.
PRINTS; PR00405; SH3DOWAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Proct kinase; 1.
ProDom; PD000006; SH2; 1.
ProDom; P0000066; SH3; 1.
SWART; SW00225; SH2; 1.
SWART; SW00219; TYRK; 1.
SWART; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily.
-!- SIMILARITY: Contains 1 SH2 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, S74141; AAB20754 1; --
EMBL, M83666; AAA41312 1; --
EMBL, S62445; CAA44218 1; --
PIR, JQ1321; JQ1321 1; --
HSSP, P08631; JBU1.
INTERPRO, IPR000719; SPCt kinase.
INTERPRO, IPR001495; SH2.
INTERPRO, IPR01452; SH3.
INTERPRO, IPR01245; Tyr pkinase.
Pfam; PF000169; pkinase; 1.
Pfam; PF00017; SH2; 1.
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SH3; 1.
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                                                                                                                        EDGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKABELLLLPGUPGGAFL 119
                                                                                                                                                        IRESOTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSEL 179
                                                                                                                                                                      63
                                                                                  82
                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-ROV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
                                                          PSRRKSLPSPSLSSSVQGQGPVTMEAERSKAT-AVALGSPPAGGPAELSLRLGEPLTIVS
                                                                                 PTSPKKLGPNSINSLPPG-----FVEGSEDTIVVALYDYEAIHREDLSFQKGDQMVVLE
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96224819; PubMed=8639560; Metzler W., Leating B., Pryor K., Mueller L., Farmer B.T. II; Metzlar W., Leating B., Pryor K., Mueller L., Farmer B.T. II; Metzler W., Lasting B., Pryor K., Mueller L., Farmer B.T. II; The three-dimensional solution structure of the SH2 domain from p55blk kinase."; 38:6201-6211(1996).
Biochemistry 33:6201-6211(1996).
In the stricted to B. Lymphoid cells.
I CHALLYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
I SIMILARITY: Belongs to the Tyr family of protein kinases. SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=90117147; PubMed=2404338;
Dymecki S.M., Niederhuber J.E., Desiderio S.V.;
"Specific expression of a tyrosine kinase gene, blk, in B lymphoid
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
                                 15;
           DB 1; Length 502;
                                 Indels
          26.0%; Score 351.5; DB 1;
40.9%; Pred. No. 6.9e-22;
live 32; Mismatches 73;
                                                                                                                                                                                                                                                                                           498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 SH2 domain. SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                       180 ADDICCLLKEPCVLQRAGPLPGK 202
                                                                                                                                                                                                                               206 KDGLCOKĽSVPCV----SPKPOK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M30903; AAA40453.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 247:332-336(1990).
                       Similarity 40.99
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily.
                                                                                                                                                                                                                                                                                           BLK_MOUSE
P16277;
          Query Match
Best Local Si
Matches 83;
                                                                                                                                                        120
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                                                                                                                                                                                                                                                                    RESULT 14
BLK_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSEVSGREYNIPSVHVGKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in kinase; Phosphorylation; Transferase; ATP-binding; domain; SH3 domain; 3D-structure; Lipoprotein.
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                                                  INTERPRO) : PROUDUSU; SHJ.

INTERPRO; IPROUD145; Tyr_pkinase.

InterPro; IPRO00245; Tyr_pkinase.

InterPro; IPRO00245; Tyr_pkinase.

InterPro; IPRO00246; Tyr_pkinase.

InterPro; IPRO00265; Tyr_pkinase.

InterPro; IPRO00265; Tyr_pkinase.

IPRINTS; PRO0017; SHJ. 1.

PRINTS; PRO0109; TYRKINASE.

PRINTS; PRO0109; TYRKINASE.

IPRODOM; PD0000065; SHJ; 1.

IPRODOM; PD0000065; SHJ; 1.

IPROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

IPROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0001; SHJ; 1.

IPROSITE; PS0001; SHJ; 1.

IPROSITE; PS0001; SHJ; 1.

IPROSITE; PS0001; SHJ; 1.

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PIR; A40092; A40092. PDB; 1BLJ; 12-MAR-97. PDB; 1BLK; 12-MAR-97. MGD; MGI:88169; Blk,

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                   MEDLINE-89123626; PubMed=3265417;
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                                                                                                                                                                                                                                                          "Structure and expression of lck transcripts in human lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90108697; PubMed=2558056;
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Vogel L.B., Arthur R., Fujita D.J.;
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Bjochim. Biophys. Acta 1264:168-172(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lymph;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                      Cell. Biochem. 38:117-126(1988)
                                                                                                                                     (Human)
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                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                               Wilson C.B.;
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Mak T.W.;
                  LCK HUMAN
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SEQUENCE OF 367-508 FROM N.A. MEDINE-88217332; PubMed-2835736; MEDINE-88217332; PubMed-2835736; Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.; Marpression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines."; Oncogene Res. 1:357-374(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89096891; PubMed=2850479; Garvin A.M.; Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.; Structure of the murine lck gene and its rearrangement in a murine lymphoma cell line.";
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MEDLINE=89313764; PubMed=2787474;
Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
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MEDLINE-20462621, PubMed-11009097,

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Ulivieri C.T.,

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MEDLINE-18189512, PubMed=11840567;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., Zvelebil M.J.;
Zvelebil M.J.;
Zvelebil M.J.;
Toluster analysis of an extensive human breast cancer cell line protein expression map database.";
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MEDLINE-9515508; PubMed-7852312;
VOGel L.B., Fujita D.J.;
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MEDLINE-87000726; PubMed=3489486;
Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
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MEDLINE=94067101; PubMed=7504174;
Vogel L.B., Fujita D.J.;
The SH3 domain of p561ck is involved in binding to phosphatidylinositel 3' kinase from T lymphocytes.";
Mol. Cell. Biol. 13:7408-7417(1993).
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J. Biol. Chem. 270:2506-2511(1995)
[15] PHOSPHORYLATION OF TYR-504.
MEDLINE=92347326; PubMed=1639064;
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80 YNIPSVHVGKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVR 135
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Proudfoot J.R., Jakes S.;
"Carboxymethyl-phenylalanine as a replacement for phosphotyrosine in SH2 domain binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Yamaguchi H., Hendrickson W.A.;
"Structural basis for activation of human lymphocyte kinase Lck upon
Lyrosine phosphorylation.";
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SUBUNT: Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/P70 through its SH2 domain.
SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER

    FUNCTION: May participate in antigen-induced T-cell activation.
    CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

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MEDLINE-96177765; PubMed-8604142;
TOTO L., Warren T.C., King J., Betageri R., Rose J., Jakes S.;
"Crystal structures of the human p561ck SH2 domain in complex with two short phosphoryzosyl peptides at 1.0-A and 1.8-A resolution."; J. Mol. Biol. 256:601-610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          K. FAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 126-220.
WEDLINE-95173978; PubMed=7532720;
Mikol V., Baumann G., Keller T.H., Manning U.M., Zurini M.G.M.,;
"The crystal structures of the SH2 domain of p561ck complexed with
two phosphonopeptides uggest a gated peptide binding site.";
T. Mol. Biol. 246:344-355(1995).
                                                                                                                                                                              [16]
**REAL CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
**MEDLINE=94203291; PubMed=7512222;
**Eck M.J., Atweell S.K., Shoelson S.E., Harrison S.C.;
**Structure of the regulatory domains of the Src-family tyrosine
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lature 368:764-769(1994)
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APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
APPLICANT: Gishizsky, Mikkail
APPLICANT: Sures, Irman G
ITILE OF INVENTION: NOVEL MEGAKARYOCYTIC FROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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39.8%; Pred. No. 1.7e-31;
iive 36; Mismatches 76;
                                                                                 US-07-820-011A-2
US-09-470-881-3
US-08-594-0447-1
US-08-655-647-1
US-08-655-647-1
US-08-470-018-7
US-08-426-509A-13
US-08-425-509A-13
US-08-325-545-13
PCT-US95-0008-13
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US-08-574-959A-5
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HRR: 7683-0074-999
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COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOCHWARE: FastSEQ Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFECATION: 435
PRIOR APPLICATION NUMBER: 08/232,545
FILING DATE: APPLICATION NUMBER: 08/232,545
FILING DATE: APPLICATION NUMBER: 08/232,545
FILING DATE: APPLICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
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Patent No. 6326469
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: DISKETTE
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep;*
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                                   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-09-555B-17
US-08-426-509A-18
US-09-457-040B-8
US-08-232-545-18
PCT-US-5-05008
US-08-426-509A-11
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US-08-232-545-19
PCT-US95-05008-19
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US-08-232-545-15
PCT-US95-05008-15
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PCT-US95-05008-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                Copyright
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Maximum DB seq
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122 ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELAD
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FTLING DATE: 24-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
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27.4%; Score 370.5; DB E
Best Local Similarity 39.8%; Pred. No. 1.7e-31;
Matches 80; Conservative 36; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION:
PRILING DATE: 24-APK-1200
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
APPLICATION NUMBER: 22-APK-1994
                                                                                                                                                                                                                                                                  515 Galveston Drive
Redwood City, California
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7683-074
                                                                                                                                                                                                          Sequence 16, Application PC/TUS9505008 GENERAL INFORMATION:
                                                                            182 DICCLLKEPCVLORAGPLPGK 202
                                                                                                               217 GLCRRLEKACI ----SPKPOK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-APR-1994
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: COCUZZI, LANIA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)869-9741
                                                                                                                                                                                                                                                                                                                              Wissenschaften E.V.
Hofgarten Str. 2
Munchen 80539
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Germany
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
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                                                                                                         6 SRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 65
                                                                                                                                                         122 ESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELAD 181
                                                                              GDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLLPGNPGGAFLIR 121
                               38 SNKQQRPVPE-SQLLPGQRPQTKDPBEQGDIVVALYPYDGIHPDDLSFKKGBKMKVLEEH 96
      6 SRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSED 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 SNKOORPVPE-SOLLPGORFQTKDPEEQGDIVVALYPYDGIHPDDLSFKKGEKMKVLEEH
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Mkhail
APPLICANT: Giehizeky, Mkhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 512;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.4%; Score 370.5; DB 439.8%; Pred. No. 1.7e-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: US/08/232,545
FILING DATE: 22-APR-1994
TORNEY/ATTON: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       182 DICCLLKEPCVLQRAGPLPGK 202
                                                                                                                                                                                                                                                                          217 GLCRRLEKACI----SPKPOK 233
                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENY INFORMATION:
NAME: CORUZZI, LGURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPACK: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,742
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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ZIP: 10036
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy
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Best Local Similarity
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Novel Megakaryocytic Protein Tyrosine
Kinases
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LAUDRESS:

SIREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A.
ZIP: 10036
OWHUTER PT.
                                                                                                                                                    Sequence 17, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
26.6%; Sca
Best Local Similarity 41.6%; Pra
Matches 77; Conservative 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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217 SVPCM 221
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                                                                                            RESULT 5
US-08-232-545-17
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      ESQIRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSBLAD 181
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ullrich., Axel
APPLICANT: Ullrich., Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mixhail
APPLICANT: Gishizsky, Mixhail
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CLASSIFICATION NUMBER: US/08/426,509A FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRICR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/232,545
FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: COTUZZI, LAURA A REGISTRATION NUMBER: 30,742
REFERENCE DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08426509A
Patent No. 6256469
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
                                                                                                                           182 DICCLLKEPCVLQRAGPLPGK 202
                                                                                                                                                                                             217 GLCRRLEKACI ---- SPKPOK 233
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 505 amino acids
amino acid
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Best Local Similarity 41.6%
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US-08-426-509A-17
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72 LSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEBLLLLPGNPGGAFLIRESQTRR 127
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APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%; Score 360.5; DB 4; Length 505; 41.6%; Pred. No. 2e-30; tive 31; Mismatches 70; Indels 7;
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOARE:
APPLICATION NOARE: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULE A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 7683-050
TELECOMMULICATION:
TELECOMMULICATION:
TELEPHONE: (212)790-9090
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PCT-US95-05008-17
Sequence 17, Application PC/TUS9505008
GENERAL INFORMATION:
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GENERAL INFORMATION:
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Pred. No. 2e-30;
1; Mismatches 70; Indels 7
                                                                         APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PALLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
                    S Galveston Drive
dwood City, California 94063-4720
lited States of America
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%; SCO
41.6%; Pre
ltive 31;
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 41.61
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        STREET: 1155 ... CITY: New York STATE: New York
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US-08-426-509A-19
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Sequence 19, Application US/08426509A Patent No. 6326469

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92 -HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRI 150
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Patent No. 6506578
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Iras, Iras Gishizsky, Mikhail
APPLICANT: Nures, Iras Gishizsky, Mikhail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 499;
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APPLICANT: Ullrich,, Axel
APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.5%; Score 344.5; DB 4; Best Local Similarity 36.0%; Pred. No. 1.1e-28; Matches 80; Conservative 32; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COCIUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELEPHONE: 212-790-909
TELEFAK: 212-869-9741
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERESTICS:
                                                                                                                            NOWIMER UP SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STRATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILLING DATE: 21-APP-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: 08/232,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 6326469e
US-08-426-509A-19
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US-08-232-545-19
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US-09-862-154-1

| Sequence | Application US/09862154 |
| Patent No. 6589758 |
| GENERAL INFORMATION |
| APPLICANT: Zhu, Xiaotian |
| TILLE OF INFORMATION |
| TILLE OF INFORMATION |
| FILLE REFERENCE: Acty. Docket No. 6589758: A-749 |
| CURRENT PLINIG DATE: 2001-05-21 |
| NUMBER OF SEQ ID NOS: 1 |
| SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                           CZIP: 10036

CZPUTIST 10036

MEDIUM TYPE: Ploppy disk

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURSITING DATE: 24-APR-1995

CLASSIFICATION NUMBER: PCT/US95/05008

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545

FILING DATE: 22-APR-1994

CLASSIFICATION: DATA:
ATTONREY/AGENT INPORMATION:
ATTONREY/AGENT INPORMATION:
NAME: COLUZZ, Laura A.
REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

RELEEPROR (212) 790-909

TELEFRAM: (212) 790-909

TELEFRAM: (212) 899-9741

TELEFRAM: 499 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids
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.1e-28;
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36.0%; Pred. No. 1.1e
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGSLPSRRKSLPSPSLSSSVQGQGPV---
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.0%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 1
| LENGTH: 508
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-09-862-154-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                         New York
: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                            COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-05008-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 344.5; DB 4; Length 499; 36.0%; Pred. No. 1.1e-28; tive 32; Mismatches 73; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV 192
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ZIP: 10036
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, Laura A 30,742
REFERENCE/DOCKET NUMBER: 36,742
REFERENCE/DOCKET NUMBER: 36,742
REFERENCE/DOCKET NUMBER: 36,742
REFERENCE/DOCKET NUMBER: 1683-050
TELECOMUNICATION NUMBER: 7683-050
TELECOMUNICATION NUMBER: 1969
TELECOMUNICATION NUMBER: 1969
TELECOMUNICATION NUMBER: 1969
TELECOMUNICATION NUMBER: 1969
TELECOMUNICATION PROPRATION:
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Redwood City, California 94063-4720
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGSLPSRRKSLPSPSLSSSVQGQGPV-----
                                   STREET: LISS Avenue of the Americas CITY: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wissenschaften E.V
Hofgarten Str. 2
Munchen 80539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 19:
SEQUENCE CHARACTERISTICS:
IENGTH: 499 amino acids
TYPE: amino acid
   TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CAURESPONDENCE ADDRESS:
CADDRESSEE: Pennie & Edmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 36.0%
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
PCT-US95-05008-19
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                                                                                                                  1 MGLLSSKRQ-----VSEKGKGWSPVKIRTQDKAPPPLPPLVVFNHLAPPSPNQDPDEEE 54
                                                                                                                                                                                                                                        92 -HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRI
                                  37; Gaps
Length 499;
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49 VIYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 YNIPSVHYGKVS----HGWLYEGLSREKAERLLLLPGNPGGAFLIRESQTRRGSYSLSVR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
                                                                                                       169 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK 228
80 YNIPSVHVGKVS----HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 VIMEAERSKAT-----AVALGSFPAGGPAELSIRIGEPLIIVSEDGDWWTVLSEVSGRE
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                                                                                                                                                                                                            Sequence 18, Application US/08426509A

Sequence 18, Application US/08426509A

Batent No. 632469

GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
APPLICANT: Gishizsky,, Mikhail
APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sinsten, TYROSINE MASES
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie, E Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York,
STATE: NY
COUNTRY: USA
COUNTRY: USA
ZIP: 10336-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
25.1%; Score 340; DB 4; L
Best Local Similarity 40.6%; Pred. No. 3.5e-28;
Matches 73; Conservative 26; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOSSOFTWARE: FastSED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILLING DATE: 21-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFFLIANT NOTES 12 - APR 1995
CLASSIPICATION A 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTONEY ABORT INFORMATION:
NAME: COTIZZI, LAULA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 amino acids
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OPERATING SYSTEM:
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US-08-426-509A-18
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US-08-426-509A-18
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                                                                                                                                                                                                                                                                                             168 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK 227
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                                                                                                           26 VIMEAERSKAT-----AVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGRE 79
                                                                                                                                           48 VIYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE
                                                                  Gaps
                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 509; 3.5e-28;
                              Length 508;
                         25.1%; Score.340; DB 4; Length 500
40.6%; Pred. No. 3.5e-28;
tive 26; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09039555B
Patent No. 6033856
GENERAL INFORMATION:
APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
TAPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
CLASSITCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19710643.9
FILING DATE: 14-MAR-1997
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALUNESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 STRIY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.1%; Score 340; 40.6%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016779/0131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 509 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.69
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5399
                              Query Match
Best Local Similarity 40.6
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. str
.....b.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
COMPUTER: Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18.
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acids
STRANDEDINESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                             Best Local Similarity 40.6%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212)869-9741
                         unknown
                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
PCT-US95-05008-18
                                                                         J MOLECULE IN US-08-232-545-18
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                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 VTYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 YNIPSVHYGKVS----HGWLYEGLSREXAEELLILLPGNPGGAFLIRESQTRRGSYSLSVR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 VIMEAERSKAT-----AVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGRE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08232545
Patent No. 6506578
GENERAL INFORMATION:
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                          25.1%; Score 340; DB 4; Length 509; 40.6%; Pred. No. 3.5e-28; tive 26; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR.1994
CLASSIFICATION: 435.
                                                            GENERAL INFORMATION:
APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Bellon, Steve
ITILE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VERT/98-14
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
                      Sequence 8, Application US/09457040B
Patent No. 6387641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALCANDA
NAME: COTUZZI, LEURA A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 7683.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 40.63
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
US-09-457-040B-8
                                                                                                                                                                                                                                                                                                                                                                          US-09-457-040B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-232-545-18
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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'n
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                                                                                                                                                                                   80 YNIPSVHVGKVS----HGWLYEGLSREKAEBLLLLPGNPGGAFLIRESQTRRGSYSLSVR
                                                                                          26 VTMEAERSKAT----AVALGSPPAGGPAELSLRIGEPLTIVSEDGDWWTVLSEVSGRE
                                                                                                                                    49 VIYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sugen, Inc.
APPLICANT: Sugen, Inc.
APPLICANT: S15 Galveston Drive
APPLICANT: Redwood City, Callifornia 94063-4720
APPLICANT: Wissenschaften E.V.
APPLICANT: Wissenschaften E.V.
APPLICANT: Munchen 80539
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Pennie £ F.J.
STRRFFT.
  Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCES
CORRESPONDENCES
COUNTY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: PEM PC-DOS/MS-DOS
SOFTWARE: PATONIUM Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RELING DATE: 24-APR-1995
25.1%; Score 340; DB 4;
40.6%; Pred. No. 3.5e-28;
tive 26; Mismatches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-APR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
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PCT-US95-05008-18
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		_	10	M	10	m
	79	108	13	16	19	22
Gaps	EVSGRE	LTTGQE	YSLSVR	FSLSVR	PCVLOR	PCQTQK
9;	WWTVLS	WWKAQS	OTRRGS	ESTAGE	CCLLKE	CTRLSF
Query Match 25.1%; Score 340; DB 5; Length 509; Best Local Similarity 40.6%; Pred. No. 3.5e-28; Matches 73; Conservative 26; Mismatches 71; Indels 10; Gaps	26 VIMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWMTVLSEVSGRE 79	49 VIYEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE 108	80 YNIPSVHYGKVSHGWLYEGLSREKAEELLLLEPGNPGGAFLIRESQTRRGSYSLSVR 135	109 GPIPFNFVAKANSLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLRESESTAGSFSLSVR 168	136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195	169 DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCGTQK 228
3 5; I 9-28; 71;	LRLGEPI	FEKGEQI	LLPGNPC	LAPGNT	LOALVDE	 LHELVRI
340; DJ No. 3.50 natches	GPAELS:	SHDGDLG	EKAEELL	KDAERQL	PRLTFPS	PRITEPG
Score Pred. 1	ALGSFPA(L	TYEGLSE	FFKNLSR	NGWLYIS	NGGFYIS
25.1%; Score 340; DB 5; 40.6%; Pred. No. 3.5e-28; ive 26; Mismatches 71	AV	TODNEVI	H	SLEPEPW	IYRIHCLD	: YKIRNLD
Query Match Best Local Similarity Matches 73; Conservat	ERSKAT-	SNPPASE	VHVGKVS	HEVAKAN	SWDRIRE	:::
Simila 3; Co	VTMEA	VTYEG	YNIPS	GFIPF	LSRPA	DFDQN
Match ocal 9 s 73	26	49	80	109	136	169
Query Match Best Local S Matches 73	S -	٥	>-	Ω	>-	.0
	8	qq	ő	qa	හි	qq

Search completed: February 20, 2004, 09:34:03 Job time : 47 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	February 20, 2004, 09:32:17 ; Search time 593 Seconds (without alignments) 92.936 Million cell updates/sec
w model	9:32:17
using s	2004, 0
OM protein - protein search, using sw model	February 20,
OM protein -	Run on:

US-09-939-853A-75

1353 1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA 261 Perfect score: Sequence:

Scoring table:

809742 segs, 211153259 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database ;

Published Applications AA:*

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2: (cgn26/prodata/2/pubpaa/US07_PUBCOMB.pep:*

3: (cgn26/prodata/2/pubpaa/US06_NEW_PUB.pep:*

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9: (cgn26/prodata/2/pubpaa/US08_NEW_PUB.pep:*

10: (cgn26/prodata/2/pubpaa/US08_PUBCOMB.pep:*

11: (cgn26/prodata/2/pubpaa/US08_PUBCOMB.pep:*

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13: (cgn26/prodata/2/pubpaa/US08_PUBCOMB.pep:*

14: (cgn26/prodata/2/pubpaa/US08_PUBCOMB.pep:*

15: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:*

16: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:*

16: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:*

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18: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:*

19: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:*

10: (cgn26/prodata/2/pubpaa/US107_PUBCOMB.pep:* /cqn2 6/ptodata/2/pubpaa/US60 PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	Sequence 954, App	Sequence 1916, Ap	Sequence 64, Appl	Sequence 64, Appl	Sequence 3, Appli	Sequence 952, App		Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 162, App	Seguence 17, Appl	Seguence 17, Appl	Sequence 17, Appl
	ΔI	US-10-043-649-2	US-09-867-550-954	US-09-867-550-1916	US-09-870-759-64	US-09-751-708A-64	US-10-043-649-3	US-09-867-550-952	US-10-394-322A-42	US-09-977-269-16	US-09-977-260-16	US-09-977-261-16	US-10-116-275-162	US-09-977-269-17	US-09-977-260-17	US-09-977-261-17
	DB	14	თ	თ	თ	10	14	σ	15	0	σ	10	15	σ	σ	10
	Query Match Length DB	261	159	113	276	276	276	96	511	512	512	512	512	505	505	505
≯ ∘	Query	9.66	61.0	43.3	35.6	35.6	35.6	33.4	27.4	27.4	27.4	27.4	27.4	26.6	26.6	26.6
	Score	1347	826	586	481,5	481,5	481.5	452.5	370.5	370.5	370.5	370.5	370.5	360.5	360.5	360.5
	Result No.	п	7	e	4	Ŋ	9	7	œ	σι	10	11	12	13	14	15

Sequence 2, Appli	Sequence 31, Appl		186,	e 28,	19,	13	e 19,	e 41,	18,	18,	e 18,	, 1,	95,	212,	213,	121,	122,	e 30,	11,	11,	e 11,	14,	14,	e 14,	4	68	15,	15,	e 15,
US-10-193-7	15 US-10-394-322A-31	5 US-10-394-3	Ħ	.0-366-288-	4	US-09-977-260-1	US-09-977	10-394-3	0 US-09-977-269-18	19-977-260-1	T6-60-SD	4 US-10-21	US-09-771-161A-9	US-09-771	US-09-771-161A-21	12	US-09-771-161A-12	0-394	ᅼ	-216-60-SD	0 US-09-977-261-	9 US-09-977-269-14	US-09-977-260-1	US-09-977	14 US-10-298-377A-4	US-10-394-322A	-776-6	US-09-977-260-1	10 US-09-977-261-15
•	526	• •		209			499	508	509	509	509								537	-				543	543	543	529	529	529
26.6	26.6	26.1	26.1	25.7	25.5	25.5	25.5	25.1	Ŋ	25.1	25.1	ß	23.8	23.5	23.5	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.1	23.1	23.1
360.5	360.5	352.5	352.5	348	344.5	344.5	44	340	340	340	340	340	ς.	18.	18	Н	15.	15.	315.5	15.	15	315.5	15	15.	ц В	15.	ч	12.	312.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US20030059924Alel Inhibitor of Antigen-receptor (
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sheng, Ning
; TITLE OF INVENTION: Cloning of a No. US20030059924A1el Inhi
; TITLE OF INVENTION: Cloning of a No. US20030059924A1el Inhi
; TITLE OF INVENTION: Retroviral-based Functional Screen
; FILE REFERENCE: A-70219-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/043,649
; CURRENT FILING DATE: 2002-01-10
; PRIOR PILING DATE: 2001-01-10
; NUMBER OF SEQ ID NOS: 3
; SOUTWARE: Patentin version 3.1
; SEQ ID NO 2
; LEMOTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.6%; Score 1347; DB 14; Best Local Similarity 99.6%; Pred. No. 2e-124; Matches 260; Conservative 0; Mismatches 1;
Sequence 2, Application US/10043649
Publication No. US20030059924A1
GENERAL INFORMATION:
                                                                           APPLICANT: Holland, Sacha J.
APPLICANT: Mendenhall, Marcy K.
APPLICANT: Pardo, Jorge
APPLICANT: Spencer, Collin
APPLICANT: Fu, C. Alan
APPLICANT: Luo, Ying
                                                                                                                                                                                                                       Payan, Donald G.
Mancebo, Helena S.Y.
                                                                                                                                                                                                                                                                                                                       Shen, Mary
Liao, X. Charlene
                                                                                                                                                                                                                                                                                        Zhou, Xiulan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-043-649-2
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1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLT 60

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Sequence 64, Application US/09870759

Sequence 64, Application US/09870759

Batent No. US20020177551A1

GENERAL INFORMATION:
APPLICANT TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT FILING DATE: 2000-01-14

PRIOR PLILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 IHCLDNGWLYISPRLTFPSLQALVDHYSBLADDICCLLKEPCVLQRAGPLPGKDIPLPVT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 EPCVLQRAGPLPGKDIPLPVTVQRTPLNWKELDSSLLFSEAATG------EESLLSEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 WIVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQRAGFLPGKDIPLPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 VORTPLNWKELDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VQRIPLNWKRLDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                       ; IOCRTION: (1)
; OTHER INFORMATION: Wherein Xaa may be any one of Arg or Gly or US-09-867-550-1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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; Pred. No. 4.8e-39;
43; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 6.8e-50;
Matches 112; Conservative 0; Mismatches 0;
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2140-2013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.3%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-870-759-64
                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT LOCATION: (1)
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Patent No. US20020082206A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynuclectides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09-09-20
CURRENT APPLICATION NUMBER: US/09-09-20
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 954
LENGTH: 159
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     1 MGSLPSRRKSLPSPSLSSSVQGQGPVTMBAERSKATAVALGSFPAGGPAELSLRLGEPLT
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ORGANISM: Homo sapiens
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Best Local Simil
Matches 158; C
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US/08/80 427
PRIOR APPLICATION NUMBER: US/08/80 427
PRIOR APPLICATION NUMBER: US/08/80 427
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 952
LENGTH: 96
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                                                                                                                                                                       35.6%; Score 481.5; DB 1.40.3%; Pred. No. 4.8e-39; Live 43; Mismatches 85
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 76.8%
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Best Local Similarity 40.33
Matches 102; Conservative
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US-09-867-550-952
                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-043-649-3
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                                          SEQ ID NO 3
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APPLICANT: Zhou, Xiulan
APPLICANT: Shen, Mary
APPLICANT: Liao, X. Charlene
APPLICANT: Sheng, Ning
TITLE OF INVENTION: Cloning of a No. US20030059924Alel Inhibitor of Antigen-receptor
TITLE OF INVENTION: Retroviral-based Functional Screen
TITLE OF PREDICATION NUMBER: US/10/043,649
CURRENT APPLICATION NUMBER: US/10/043,649
                                                                                                Sequence 64, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TILLE REPERENCE: 751708
FILLE REPERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 1090-110-15
PRIOR PIPLICATION NUMBER: US 60/173,371
NUMBER OF SEQ ID NOS: 166
SOUTHARE: PatentIn version 3.1
LUNGTH: 276
LUNGTH: 276
LUNGTH: 276
LUNGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10043649
Publication No. US20030059924A1
GENERAL INFORMATION
APPLICANT: Holland, Sacha J.
APPLICANT: Mendenhall, Marcy K.
APPLICANT: Pardo, Jorge
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Fu, C. Alan
Luo, Ying
Payan, Donald G.
Mancebo, Helena S.Y.
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    230 RESIASYLSLTSE 242
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ORGANISM: Homo sapiens
                                                                                       JS-09-751-708A-64
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US-10-043-649-3
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Best Local
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APPLICANT:
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217 GLCRRLEKACI----SPKPQK 233
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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US-09-977-260-16
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US-09-977-261-16
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US-09-977-260-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :: | | : | | : | | : | | : | | 37 SNKQQRPVPE-SQLLPGQRFKYGEKWKVLEEH 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09971269
; Sequence 16, Application US/09971269
; Patent No. US20020082037A1
; GENERAL INFORMATION:
    APPLICANT: ULLRICH, AXEL
    APPLICANT: ULLRICH, AXEL
    APPLICANT: GISHIZKY, MIKHAIL
    APPLICANT: GISHIZKY, MIKHAIL
    APPLICANT: WOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
; FILE REFERENCE: 038602/1260
; CURRENT APPLICATION NUMBER: US/09/977,269
; CURRENT FILING DATE: 1094-04-22
; PRIOR PILING DATE: 1994-04-22
; NUMBER: OS EQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                             5; DB 15; Length 511;
1e-27;
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                                                          Sequence 42. Application US/10394322A

Publication No. US20030232391A1

GENERAL INFORMATION:
APPLICANT: SUBSESS PHARMACEUTICALS, INC.
APPLICANT: STRESS PHARMACEUTICALS, INC.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT FILING DATE: 2003-03-20

PRIOR FILING DATE: 2002-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 511
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39.8%; Pred. No. 1e-2
live 36; Mismatches
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Best Local Similarity 39.8%
Matches 80, Conservative
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ORGANISM: Homo sapiens
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Matches 80; Conserv
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US-09-977-269-16
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; Publication No. US20030054527A1
; Publication No. US20030054527A1
; GENERAL INFORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: ULLRICKY, MIKHAIL
APPLICANT: ULIRICKY, MIKHAIL
APPLICANT: ULIRICKY, MIKHAIL
APPLICANT: US/08/01/125
CURRENT GISHIKKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
CURRENT APPLICATION NUMBER: US/09/977,261
CURRENT APPLICATION NUMBER: US/09/977,261
CURRENT FILING DATE: 1994-04-22
MUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09977260
Publication No. US20020192790A1
GENERAL INFORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: ULLRICH, AXEL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOWER MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
CURRENT PELING DATE: 2001-10-16
PRIOR PLING DATE: 1994-04-22
PRIOR APPLICATION NUMBER: 08/222,545
PRIOR APPLICATION NUMBER: 08/222,545
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128 GSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 PSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTV
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     Sequence 17, Application US/09977269; Patent No. US20020082037A1.
GENERAL INFORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: GOMES, INMOGRED:
TITLE OF INVENTION NOWER: US/09/977,269
CURRENT APPLICATION NUMBER: US/09/977,269
CURRENT FILING DATE: 2001.10-16
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOUTHWARE: Patentin Ver. 2.1
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SOFTWARE: Patentin Ver.
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US-09-977-260-17
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ORGANISM: Homo sapiens
US-09-977-269-17
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LENGTH: 505
TYPE: PRT
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CURRENT PILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
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39.8%; Pred. No. 1e-27;
tive 36; Mismatches 76; Indels
                                                                                                                                                                                                76; Indels
                                                                                                                                                  27.4%; Score 370.5; DB 10; 39.8%; Pred. No. 1e-27;
                                                                                                                                                                                                      36; Mismatches
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Best Local Similarity 39.8
Matches 80; Conservative
                                                                                                                                                                                                      80; Conservative
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ORGANISM: Homo sapiens
; SEQ ID NO 16
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-261-16
                                                                                                                                                     Query Match
Best Local Similarity
Matches 80; Conserv
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Gaps

Indels

Length 505;

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LSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRR 127
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Sequence 17, Application US/09977260
Publication No. US20020192790A1
GENERAL INFORMATION
AND ARE
APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
CURRENT APPLICATION NUMBER: US/09/977,260
CURRENT APPLICATION NUMBER: 08/23,545
PRIOR APPLICATION NUMBER: 08/22,545
PRIOR FILING DATE: 1994-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 505;
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RESULT

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                                                         128 GSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLL 187
                                                                                   40 PGPNSHNS----NTPGIREAGSEDIIVVALYDSTHHEDLSFQKGDQMVVLEESGEWWKA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 PSPSLSSSVQQQPVTMBAERSKATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTV 71
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Publication No. US20030054527A1

GENERAL INFORMATION:

APPLICANT: ULLRICH, AXEL

APPLICANT: ULLRICH, AXEL

APPLICANT: GISHIZKY, MIGHAIL

APPLICANT: GISHIZKY, MIGHAIL

APPLICANT: GISHIZKY, MIGHAIL

APPLICANT: GISHIZKY, MIGHAIL

APPLICANT: ULLRICH, AXEL

CURRENT GISHIZKY, MIGHAIL

FILE REFERENCE: 038602/1259

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: US/09/977,261

CURRENT FILING DATE: 1994-04-22

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 17

LENGTH: 505
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26.6%; Score 360.5; DB 10; Length
Best Local Similarity 41.6%; Pred. No. 9.6e-27;
Matches 77; Conservative 31; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-261-17
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                    1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
5: Sp_mammal:*
5: Sp_mammal:*
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5: Sp_organalle:*
5: Sp_hage:*
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sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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sp_plant: *
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q7tmx7 mus musculu	Q7t0u4 xenopus lae	Q7t3x8 gallus gall		Q9ddk6 salmo salar	Ol3064 xenopus lae	Q96in1 homo sapien	Q8k2m8 mus musculu	Q95m32 hylobates s	Q91x65 mus musculu	Q95kr7 saimiri sci		Q62844 rattus norv	O93411 xenopus lae	Q99pwl rattus norv	Q85466 avian sarco
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SUMMARIES ID	07 TMX 7	Q7T0U4	Q7T3X8	QBCEIO	Q9DDK6	013064	INI960	Q8K2M8	Q95M32	Q91X65	Q95KR7	Q7ZYH5	Q62844	093411	TMd660	085466
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% Query Match Length DB	259	266	282	491	502	488	505	499	509	509	509	519	537	496	541	812
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SCO	1028	583	467.5	375	366.5	361.5	352.5	344.5	340	338.5	328	320.5	315.5	313.5	309.5	309
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Q7ZYK3 Q63206 Q8CBP1 Q16248 Q95M31	Q8K2A3 Q8AWF1 Q9Y1Z1 O77050	Q8BGMU Q8C762 Q64817 Q8WQM5	Q8QGJ9 Q85477 Q64994 Q8N5D7	Q80XU2 Q86VB9 Q86VB9 Q64993 Q86363	092806 Q9JJ10 Q8WSU2 Q86362 Q7ZX73
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ALIGNMENTS

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Src-like adaptor protein.
Gallus gallus (Chicken).
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Jones S.J., Marra M.A.;
                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Spleen;
                                              and mouse cDNA sec
Proc. Natl. Acad.
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**REDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Barchow K.H., Schaefer C.F., Bhat N.K., Astachench C., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer D. Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raplecton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Apramen M.J., McKernan K.J., Abramenn R.D., Mullahy S.J., Aschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A., Anderson M.C., Abey J., Helton E., Scherman M., Madan A., Rodrigues S., Sanchez A., Markelley R.W., Touchman J.W., Gremutz J., Dickson M.C., Butterfield Y.S., Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                            61 IVSEDGDWWTVLSEVSGREYNIPSVHVGKVSHGWLYEGLSREKAEELLLLPGNPGGAFLI 120
                                                                                                                                                                                                                                                                                                                                                                                                           60 IISEDGDWWTVQSEVSGREYHMPSVXVAKVAHGWLYEGLSREKAEELLLLPGNPGGAFLI 119
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                                                                                                                                                                                                        Gaps
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Kapothetical protein clawed frog).

Kenopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                           4,
                                                                                                                                                      259;
                                                                                                                                                    76.0%; Score 1028; DB 11; Length 79.4%; Pred. No. 1.8e-84; ive 16; Mismatches 34; Indels
  Strausberg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL/SenBank/DDBJ databases. EMBL; BCOSEGES; AAHS2655.1; -. Hypothetical protein. Hypothetical protein. SEQUENCE 259 AA; 28495 MW; F078D1FBB720B7CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                    Query Match
Best Local Similarity 79.4%
Matches 208; Conservative
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more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euwaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Lebigot I., Gardellin P., Lefebvre L., Beug H., Ghysdael J.,
Tran Quang C.;
"Cloning of the avian Src-like adaptor protein cDNA.";
"Conning of APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY278230; AAR34689.1; -
SEQUENCE 282 AA; 31988 MW; 85EA8B1D8986D416 CRC64;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                 Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS6035, AAHS6035.1; -.
Hypothetical protein.
SEQUENCE 266 AA; 30303 MW; EF20A453A4CD673B CRC64;
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                              Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                               Query Match
43.1%; Score 583; DB 13;
Best Local Similarity 47.5%; Pred. No. 2.5e-44;
Matches 125; Conservative 48; Mismatches 80
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       and initial analysis of
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234
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STRAIN=CS7BL/619; TISSUE=Pancreas;
MPDILIN=22354683; PubMed=12466851;
The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
TARABLYSIS of the mouse transcriptome based on functional annotation of
60,770:full-length cDNAs.";
Nature 420:563-573(2002).
                                             PCVLQRAGPLPGKDIPLPVTVQRTPLNWKEL-----DSSLLFSEAATGEESLLSEGLR
                                                              R MGD; MGC08125 JAC65731; P. R MGD; MGC08125 JAC65731; P. R MGD; MGC08125 JAC65731; P. R MGD; MGC08005524; Firstein serine/threonine kinase activity; IEA. GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA. GO; GO:0004713; F:protein-serine/threonine kinase activity; IEA. GO; GO:0004713; F:protein-serine/threoning cascade; IEA. GO; GO:0006468; P:protein amino acid phosphorylation; IEA. InterPro; IPR001229; Srot kinase.

R InterPro; IPR001229; Srot kinase.
R InterPro; IPR001245; JYT pkinase.
R InterPro; IPR001245; TYT pkinase.
R InterPro; IPR001245; TYT pkinase. AS. Pfam; PF00017; SH2: 1.
                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCPI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
27.7%; Score 375; DB 11; Length 491;
Best Local Similarity 39.4%; Pred. No. 3.4e-25;
Matches 85; Conservative 35; Mismatches 78; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56309 MW; 2C86DB46AA4B6AAB CRC64;
                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R PROSITE; PSOO107; PROTEIN KINASE ATP; 1.
R PROSITE; PSOO11; PROTEIN_KINASE_DOM; 1.
R PROSITE; PSOO109; PROTEIN_KINASE_TYR; 1.
PROSITE; PSOO015; SH2; 1.
PROSITE; PSOO02; SH3; 1.
                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0461; SH2DOMAIN.
PRINTS, PRO0452; SH3DOMAIN.
PRINTS, PRO0109; TYRKINASE.
PRODOM; PD000001; Proc_kinase; 1.
ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                        QBCEIO;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYKK; 1.
                                                                                                                          ||:: |:|| :
235 ESIASYLSLTGD 246
                                                                                                       243 ESLSFYISLNDE 254
                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                Yamaguchi sarcoma viral
                                                                                                                                                                                                                                                                                                              musculus (Mouse)
                    124
                                               190
                                                                                                                                                                                                           Q8CEIO
                                                                                                                                                                               RESULT 4
                                                                                                                                                                                             QBCEIO
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1 MGSLPSRRK-SLPSPSLSSSVQ-----GQGPVTMEAERSKATAVALGSFPAGGPAE 50

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78; Indels 18;

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                                                          51 LSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEE 106
                                                                                             107 LILLPGUPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTF 166
                                                                                                                                                                                                                 1 MGCIKSKRKDNLNDDEVDSKTQPVPEFHLLPGQRFQTKDPEEQGDIVVALYPYDGIHPDD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; FSDUOUZ; SH3; 1.
ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SEQUENCE 502 AA; 56600 MW; 82DF0D677AA99980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordvik I., Male R.;
"A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OL-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
51-OGT-2003 (TrEMBLrel. 25, Last annotation update)
52-C-family tyrosine kinase SCK.
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R GG) GG:000524; FAIP binding; IEA.

R GG) GG:000524; FIAIP binding; IEA.

R GG) GG:000413; F:Protein-tyrosine kinase activity; IEA.

R GG; GG:000742; F:transferase activity; IEA.

R GG; GG:000742; F:intracellular signaling cascade; IEA.

R GG; GG:000648; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00019; Prot. kinase.

R InterPro; IPR00145; Pyr_pkinase.

R InterPro; IPR00145; Tyr_pkinase.

R InterPro; IPR00166; Tyr_pkinase.

R Pfam; PR00017; SH3; 1.

R Pfam; PR00017; SH3; 1.

R PRINTS; RR00401; SH2DOMAIN.

R PRINTS; RR00109; TYRKINASE.

R ProDom; PD000001; Prot. kinase; 1.

R Prodom; PD000001; Prot. kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match

27.1%; Score 366.5; DB 13; Length
Best Local Similarity 41.9%; Pred. No. 2.1e-24;
Matches 80; Conservative 29; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF321110; AAG38611.1; -.
                                                                                                                                                                                                                                                                                                                                                   181 PCISDMIKHYQKQSDGLCRRLEKACI----SPKPQK 212
                                                                                                                                                                                                                                                                                                     167 PSLOALVDHYSELADDICCLLKEPCVLORAGPLPGK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 AA.
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PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SMART; SM00326; SH3; 1.
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85 VHVGKVS----HGWLYEGLSREKAEELLLLPGUPGGAFLIRESQTRRGSYSLSVRLSRPA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 PPDEHLDEDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSLVTGREGYVPS
                                                                 53 LRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELL
                                                                                                   1 MGCIKSKTDNPRDAMGKNNPASRTPSLLPGQ-KMIQDIEEQGNIVIALYPYQGIHEDDLS
                                                                                                                                                                                         109 ILPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0004713; F:Drotein-tyrosine kinase activity; IEA.
GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO: 0007242; P:intransferase activity; IEA.
GO; GO: 0007242; P:intransferase activity; IEA.
GO; GO: 0007468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00719; Prot kinase.
InterPro; IPR001245; SH3.
InterPro; IPR001245; SH3.
InterPro; IPR001245; Tyr pkinase.
Fram; PF00017; SH2.
IPEAM; PF00017; SH2. 1.
IPEAM; PF00017; SH3: 1.
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26.1%; Score 352.5; DB 4; Length 505;
Best Local Similarity 43.6%; Pred. No. 3.8e-23;
Matches 75; Conservative 24; Mismatches 68; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007311; AAH07371.1; -.
EMBL; BC032413; AAH32413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aypothetical protein; ATP-binding; Kinase; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 AA; 57706 MW; B5F739BEF8389176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 19, Last agguence update) Hypothetical protein (B lymphoid tyrosine kinase). Hypothetical protein (B lymphoid tyrosine kinase).
                                                                                                                                                                                                                                                                                                                                                                 180 INEMIQHYQKQADGLCRKLDKPCF----SPKPQK 209
                                                                                                                                                                                                                                                                                                                        169 LOALVDHYSELADDICCLLKEPCVLORAGPLPGK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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ProDom; PD000093; SH2; 1.
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PRINTS; PR00452; SH3DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Blood, and Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyrosine-protein kinase
SEQUENCE 505 AA; 577
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                                                                                                          132 LSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPC 191
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          STGPSVPSDGP-----ESIAIALYDYEGINEGDLGFKKGDKLKILQESGEWWRAQSI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinase, SH3 domain, Transferase, Tyrosine-protein kinase
88 AA, 55794 MM, B7E70668B6EA92B2 CRC64;
                                                                           75 VSGREYNIPSVHVGKVS---HGWLYEGLSREKABELLLLPGGNPGGAFLIRESQTRRGSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukami Y., Funabiki K., Sato K.,
"Nucleotide sequence of Xenopus Lyn protein tyrosine kinase.";
Submitted (APR-1997) to the EMBL/GenBark/DDBJ databases.
-i- SIMILARIY: CONTAINS 1 SH3 DOWAIN.
EMBL, ABOO3358; BAA20078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000740; F:transferase activity; IEA.
GO; GO:000740; F:transferase activity; IEA.
GO; GO:0007468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000199; Protein amino acid phosphorylation; IEA.
InterPro; IPR00115; SH3.
InterPro; IPR001455; SH3.
InterPro; IPR001455; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase.AS.
PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00107; PROTEIN KINASE ATP; 1.
PSS0011; PROTEIN KINASE DOM; 1.
PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0401; SH2DOWAIN.
PRINTS; PR00452; SH3DOWAIN.
PRO109; TYRKINASE.
PRODOM; PD000001; Prot kinase; 1.
ProDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yn protein tyrosine kinase
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hes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase;
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                               192 VLQRAGPLPGK 202
                                                                                                                                                                                                                                                                                                                                                                           : | | | | L----SPKPQK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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SEQUENCE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
             45
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SMART; S
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Matches
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84

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49 VIYYEGSNPPASPLODNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQE 108
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                                                                                                                                                           26 VIMEAERSKAT-----AVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGRE 79
                                                                        55 RFVVALFDYAAVNDRDLQVLKGEKLQVIRSTGDWWLARSLVTGREGYVPSNFVAPVETLE 114
                                                                                                                          92 -HGWLYEGLSREKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRI 150
                         35 ATAVALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKVS--- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOOGE, S.H. domain, Transferase, Tyrosine-protein kinase.
509 AA; 57946 MW; F1BFB5C237C8DB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.1%; Score 340; DB 6; Length 509;
Best Local Similarity 40.6%; Pred. No. 5.1e-22;
Matches 73; Conservative 26; Mismatches 71; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Processor Control No. 1.

Thesis (2001), Department of Experimental Oncology laboratory, U. 1. - SIMILARITY: CONTAINS 1 SH3 DOMAIN.

REMEL, AJ320182; CAC44027.1; -.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0007242; F:Tangeferase activity; IEA.

GO; GO:0007242; P:protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:protein-tyrosine kinase activity; IEA.

GO; GO:0007242; P:protein-amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00019; Prot_kinase.

R InterPro; IPR001452; SH3.

R InterPro; IPR001454; Tyr_pkinase.

R InterPro; IPR001455; Tyr_pkinase.

R Fam; PR00017; SH2: 1.

R Pfam; PF00018; SH3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hylobates sp. (gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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                                                                                                                                                                                                                                 151 HCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCV 192
                                                                                                                                                                                                                                                                  174 RSLDNGGYYISPRITFPTLQALVQHYSKKGDGLCQKLTLPCV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TremBlrel. 19, Created)
(TremBlrel. 19, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   509 AA.
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PRINTS; PR00452; SH3DOWAIN.
PRINTS; PR00452; SH3DOWAIN.
PRINTS; PR00452; SH3DOWAIN.
ProDom; PD000003; SH2, 1.
ProDom; PD000066; SH3; 1.
SWART; SW00252; SH2; 1.
SWART; SW00225; SH2; 1.
SWART; SW00215; TYPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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PROSITE; PS50002; SH3; 1
ATP-binding; Kinase; SH3
SEQUENCE 509 AA; 5794
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01-DEC-2001 (
01-OCT-2003 (
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LCK.
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Q95M32
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-NOD; TISSUE=Spleen;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

The RANTOM Consortium,

A. The RANTOM Consortium,

A. The RANTOM Consortium,

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A. The RANTOM Consortium,

B. MEL, BC030668; AAH30661; -.

B. MEL, BC030668; AAH30661; -.

B. MEL, BC030664; FATP binding; IEA.

GO; GO:0006740; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006742; FIATP binding; IEA.

GO; GO:0006469; Pironein amino acid phosphorylation; IEA.

INTER-PRO; IPRO00290; SH2.

B. THER-PRO; IPRO01452; SH3.

INTER-PRO; IPRO0185; SH3.

INTER-PRO; IPRO0185; SH3.

INTER-PRO; IPRO0185; SH3.

B. Ffam; PF00001; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; SH2:

B. PRANTS; PRO0401; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO0405; PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.5%; Score 344.5; DB 11; Length 499; Best Local Similarity 36.0%; Pred. No. 2e-22; Matches 80; Conservative 32; Mismatches 73; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; Prococos; Sh2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00220; SH2; 1.

SMART; SM00219; TVRC; 1.

SMART; SM00219; TVRC; 1.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.

PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                           499
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                                                                                                                                                           PRT;
                                                                                                                                                                                               01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, B lymphoid Kinase.
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                    QBK2MB;
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                                                                                                         RESULT 8
Q8K2M8
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095KR7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

C STRAIN=NOD; TISSUE=Thymus;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojina Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Ohno H., Ohsato N., Okazuki X.,
A Nishi K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tanawa A., Tayanahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                            136 LSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICCLLKEPCVLQR 195
                                            DFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQK 228
109 GFIPFNFVAKANSLEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [6]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDINE=20499374; PubMed=11042159;
MEDINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; the RADASIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                        0.1050-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to lymphocyte-specific protein tyrosine kinase (2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430002B06 product:lymphocyte protein tyrosine kinase, full
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE-Thymus;
RIKEN FANTOM CONSOCTIUM;
"FUNCTIONAL ANDOLATION Of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=NDD; TISSUG=Thymus;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
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                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                     insert sequence)
                                                                                                                                 091X65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SIPSRRKSIPSPSISSSVOGOGPVTMEAERSKATAVALGSFPAGGPAELSIRLGEPLTIV 62
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AEROEMAN TISSUE-Thymus;

X MEDLINE=20530913; PubMed=11076861;

XA Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Aibhata K., Itch M., Aizawa K., Itch M., Aizawa K., Itch M., Aizawa K., Itch M., Aibhaine T., Harada A., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Harada A., Ramamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Ramamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Ramamoto R., Indew Y., Tozawa M., Ohara E., Watahiki M., Proda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., R., Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., R., Mirkeni integrated sequence analysis (RISA) system-384-format R. Genome Res. 10:1757-1771(2000).

R. EMBL; BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; AAH144.1; BR. BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; BR. BCC11444; 
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Prodom; P0000065; SH3; 1.

Prodom; P0000093; SH2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00252; SH2; 1.

SMART; SM00326; SH3; 1.

R SMART; SM00219; TYKK; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00001; SH2; 1.

R PROSITE; PS00002; SH3; 1.

R PROSITE; PS00002; SH3; 1.

R PROSITE; PS00002; SH3; 1.

R PROSITE; PS00002; SH3; 1.

R PROSITE; PS00002; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001452; SH3.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR00826; Tyr_pkinase_AS.
Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
PRINTS; PRO1009; TYRKINASE.
PRODOM; PD000001; Proc Kinase; 1.
ProDom; PD000066; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 ASDGLCTKLSRPCQTOK 228
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Fyn proto-oncogene.
Xenopus laevis (African lawed frog).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58486 MW; A790E29424AE7037 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 VEELVEHYGEFNDGLCHLLTSPCINQK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000066; SH3; 1.
SWART; SM02225; SH3; 1.
SWART; SM02220; SH2; 1.
SWART; SM02220; TYGKC; 1.
SWART; SM02219; TYGKC; 1.
PROSITE; PSC0010; PROTEIN KINASE ATP; 1.
PROSITE; PSC0010; PROTEIN KINASE ATP; 1.
PROSITE; PSC0011; PROTEIN KINASE ATP; 1.
PROSITE; PSC0001; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASB.
Probom; PD000001; Prot_kinase; 1.
Probom; PD000003; SH2; 1.
Probom; P0000066; SH3; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                        Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 AA;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                           IISSUE=Embryo;
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ID 06
AC 06
DT 01
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 VALGSFPAGGPAELSLRLGEPLTIVSEDGDWWTVLSEVSGREYNIPSVHVGKVS----HG 93
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                                                                                                                                                       Saimiri sciureus (Common squirrel monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Cebinae, Saimiri.
NCBI_TaxID=9521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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Best Local Similarity 41.4%; Pred. No. 6.2e-21;
Matches 67; Conservative 27; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 DNGWLYISPRLTFPSLOALVDHYSELADDICCLLKEPCVLQR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 DNGGFYISPRITFSGLHELVRHYTNASDGLCTRLSRPCQTQK 228
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LCk tyrosine kinase (Fragment).
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01-JUN-2003 (TrEMBLrel, 24, Created)
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Q7ZYHS
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54 RIGEPLTIV-SEDGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 ILPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 OKGEKFHIINNSEGDWWEARSLSSGNTGYIPSNYVAPMNSIOSKDWFFGKIGRKDAERLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LPSRRKSLPSPSLSSSVQG--QGP-----VTMEAERSKATAVALGSFPAGGPAELSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Gaps
KIEIN S. Strauberg R.;

KIEIN S., Strauberg R.;

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R. GO; GO:0005524; F:ATP. binding; IEA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0007424; P:intracellular signaling cascade; IEA.

R. GO; GO:0007429; P:intracellular signaling cascade; IEA.

R. GO; GO:0007429; P:intracellular signaling cascade; IEA.

R. InterPro; IPR001299; SH2.

R. InterPro; IPR001259; SH3.

R. InterPro; IPR001455; SH3.

R. InterPro; IPR001455; Tyr_pkinase.

R. InterPro; IPR001455; Tyr_pkinase.

R. Pfam; PF00017; SH2: 1.

R. Pfam; PF00017; SH2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 23.7%; Score 320.5; DB 13; Length 519; Local Similarity 36.2%; Pred. No. 3e-20; Loss 75; Conservative 37; Mismatches 76; Indels 19;
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GEPLTIV-SEDGDWWTVLSEVSGREYNIPSVHVGKV----SHGWLYEGLSREKAEELLLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 PGNPGGAFLIRESQIRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYISPRLTFPSLQ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 ĠEKFQILNŚSEGDWWBARSLTGETGYIPSNYVAPVDSIQAEBWYGKLGRKDAERQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN KINASE_DOM; 1.
PROSITE; PS00019; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
SEQUENCE 537 AA; 60702 MW; 11AE4420919DBFIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SLPSPSLSSSVQGQGPVTMEAERSKATA------VALGSFPAGGPAELSLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus:
NCBI_TaxID=10116;
                                                                                                   TISSUE-Brain;
Nemoto K., Sekimoto M., Kageyama H., Fukamachi K., Nemoto F.,
Nemoto K., Sekimoto M., Kageyama H., Fukamachi K., Nemoto F.,
Usyama T., Senba E., Tomita I.;
Expression of three type mRNAs encoding rat FYN by alternative
splicing within 5' untranslated region.";
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U35365; AAA82942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.3%; Score 315.5; DB 11; Length 537; ilarity 38.3%; Pred. No. 9e-20; Conservative 24; Mismatches 81; Indels 19;
                                                                                                                                                                                                                                     171 ALVDHYSELADDICCLLKEPC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QĽVQHÝSERÁAGLČČRĽVVPČ 246
                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Prot_kinase; 1.
ProDom; PD000003; SH2; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00219; TyrKc; 1.
 Proto-oncogene FYN.
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61 DYDGVHPGDLTFRKGDHLLLKKBSGEWWEACLISTGEBGFVPSNYVAYFNSLESEEWYFK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGSLPSR-----KKSLPSPSLSSSVQGQGP---VTM-EAERS------KATAVALG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Gaps
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
Non-receptor protein tyrosine kinase laloo.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopodina, Batrachia; Anura, Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Weinstein D.C., Marden J., Carnevali F., Hemmati-Brivanlou A.; "FGF-mediated mesoderm induction involves the Src-family kinase
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PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD0000093; SH2; I.
ProDom; PD0000093; SH2; I.
ProDom; P0000066; SH3; I.
RNART; SM00226; SH3; I.
SMART; SM00219; TYRK; I.
SMART; SM00219; TYRK; I.
SMART; PE00107; PROTEIN KINASE ATP; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS000103; PROTEIN KINASE DOM; I.
PROSITE; PS000103; PROTEIN KINASE TYR; I.
PROSITE; PS000103; RAP; I.
PROSITE; PS000103; RAP; I.
PROSITE; PS000103; RAP; I.
PROSITE; PS000104; RAP; I.
PROSITE; PS000105; RAP; I.
PROSITE; PS000105; RAP; I.
PROSITE; PS000105; RAP; I.
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SEQUENCE 496 AA; 56275 MW; 96223A6F99689965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 LYISPRITEPSLOALVDHYSELADDICCLLKEPC 191
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les 78; Conservative
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RESULT 15 Q99PW1

496 AA

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 YKIRKLDNGGYYLTTRAQFDTLQKLVKHYTEHADGLCHKLTTVCPTVKPQTQGLAKDAWE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 GWLYEGLSREKABELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIR----H 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 LPGKDIPLPVTVQR------TPLNWKELDSSLLFSEAATGEESLLSEGLRES 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Kinase; SH3; 1.
NON TER 541 541 S41 SEQUENCE 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 As: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 600 NON TER 541 AS: 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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22:9%; Score 309:5; DB 11; Length 541;
Best Local Similarity 32:0%; Pred. No. 3:2e-19;
Matches 81; Conservative 41; Mismatches 92; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0005524; F:ATE.

R GO; GO: 0005524; F:ATE.

R GO; GO: 0005524; F:ATE.

R GO; GO: 0005524; F:ATE.

R GO; GO: 0005524; F:ATE.

R GO; GO: 0007242; F:Tansferase activity; IEA.

R GO; GO: 0007242; P:intracellular signaling cascade; IEA.

R GO; GO: 0007242; P:intracellular signaling cascade; IEA.

R GO; GO: 0007242; P:intracellular signaling cascade; IEA.

R GO; GO: 0007242; P:intracellular signaling cascade; IEA.

R GO; GO: 0007242; P:intracellular signaling cascade; IEA.

R InterPro; IPR000980; SH3.

DR InterPro; IPR000452; Tyr_pkinase_AS.

DR Fam; PR00069; pkinase; 1.

DR Fam; PR00018; SH3; 1.

DR PRINTS; RR00401; SH3DOWAIN.

DR PRINTS; PR00401; SH3DOWAIN.

DR PRINTS; PR00452; SH3DOWAIN.

DR PRINTS; PR00109; TYRXINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimizu M.;
"Rat mRNA for protooncogene c-Yes.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: COTTAINS 1 SH3 DOMAIN.
EMBL, ABO37472: BAB21451.1; -.
HSSP; PO0523; 2PTK.
                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Protein tyrosine kinase c-Yes (Fragment).
     541 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD000093; SH2; 1.

Prodom; PD000066; SH3; 1.

SWART; SM00225; SH3; 1.

SWART; SM00219; TyrKc; 1.

PROSITE; PS00110; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYP; 1.

PROSITE; PS00109; PROTEIN KINASE TYP; 1.

PROSITE; PS00109; SH2; 1.
                                                                                                   (TrEMBLrel. 17, Created)
PRT;
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000093; SH2; 1.
000066; SH3; 1.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Oy 201 GlyLysAspIleProleubrovalThrValGlnArgThrProleuAsmTrpLysGluLeu 220 Db 998 GGCAAGGATRTACCCTGCTGTGATGTGAAGACACCACTACTGGAAAGAGCTG 1057 Oy 221 AspSerSerieuLeubreSerGlualaalaThrGlyGluGluSerLeuleuSerGluGly 240 Db 11058 GACAGCTCCTCTGTTTTCTGAAGCTGCCACAGGAGAGATCTCTCTC	Alignment Scores:
AX443133 DEFINITION Sequence 74 from Patent W00216599. NA linear PAT 02-JUL-2002 DEFINITION Sequence 74 from Patent W00216599. NA Linear PAT 02-JUL-2002 VERSION VERSION AX44313.1 GI:21690555 Home sapiens (human) ORGANISM Home sapiens (human) ORGANISM Home sapiens (human) REPERANCE Lurgess, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R., Shinkers, R.A., Syvek, K.A., Szekeres, E.S., Tominson, J.B., TITLE Detent: WO 0216599-A 128-FEB-2002; Lorgen Corporation (18); COR THERAPBUTICS, INC. (18) Location/Qualifiers Lurges Curage Corporation (18); COR THERAPBUTICS, INC. (18) Location/Qualifiers Location/Qualifiers Curage Corporation (18); COR THERAPBUTICS, INC. (18) Location/Qualifiers Curage Corporation (18); COR THERAPBUTICS, INC. (18) Location/Qualifiers Location/Qualifiers Location/Qualifiers Alignment Scores: Anignment Scores: Anignment Scores: Anignment Scores: Conservative: 0 Description (18); COR Matches: 0 Description	41 GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgleuGlyGluProLeuThr 60 518 GGCAGTTTCCGGCCGGCCGGCCGAGTGTCGGGGGGCCTTGACC 577 62 IleValSerGluAspClyAspTrpTrpTryTalleuSerGluVaslSerGluYrgGluTyr 80 518 ArcGrccrCaGaGATGAGAGAGTGACGGGGCGAGAGTCTCGGGCAGAGAGTTT 637 63 ArcGrccrCaGaGATGAGAGAGTGACGGGGCTGTCTCGAGCAGAGAGTT 637 64 AshleProSerValHisValGlyLyVaValSerHisGlyTrbLeuTyrGluGlyLeuSer 100 65 AshleProSerValHisValGlyLyVaValSerHisGlyTrbLeuTyrGluGlyLeuSer 100 65 AAGATCCCCAGGGGCGCAGAGAGTCTCCCATGGGTGATGAGGGCTGAGGGTT 637 65 AAGATCCCCAGGGAGAGAGAGTCTCTCTCTCTCTGAGGTGATTCCTCATCCTCATCCTCATCAGGGGGCTGAGGGTT 637 65 AAGATCCCCAGGGAGAGAGAGTGTTACTTGTTACTCTGAGGGTGTATTCTCATCCTCATCCTCATCAGTGGTGAGGGGTTACTCTCATCTCATCAGTGGTGAGGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTCTCATCAGTGGTTACTTCTCAGTGGTTACTCTCATCAGTGGTTACTTCTCATCAGTGGTTACTTCTCATCAGTGGTTACTTCTCATCAGTGGTTACTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTACTTTACTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTAC

	Cy 81 ASNILeProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100	121 361	161 SerProArgLeuThrPheProSerLeuGlnAlateuValAspHisTyrSerGluLeuAla 18	201 GlytysAspileProLeuProValThrValGlnArgThrProLeuAshTrpLysGluLeu GlytysAspileProLeuProValThrValGlnArgThrProLeuAshTrpLysGluLeu GlytysAspileProLeuProValThrValGlnArgThrProLeuAshTrpLysGluLeu GlytysAspileProCertGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrG	Oy 261 Ala 261 Db 781 GCC 783 RESULT 4 AX572845 LOCUS DEFINITION Sequence 1 from Patent WO02055707. WERSION AX572845 VERSION AX572845 VERSION AX572845.1 GI:26004935	XEXEMOLES KENNOLUS KENNOLUS CRGANISM Homo sapiens CRGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Luo, X., Payan, D.G., Mancebo, H.S., Mu, J., Zhou, X., Shen, M., Liao, X.C. and Sheng, N. TITLE Cloning of an inhibitor of antigen-receptor signaling by a retroviral based functional screen JOURNAL Patent: WO 20255/07-A 1 18-JUL-2002; Rigel Pharmaceuticals, Inc. (US) REATURES Location/Qualifiers Jource Jourc
	Oy 161 SerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla 180	GlyLysabpileProleuProValThrValGlnArgThrProleuAsnTrpLysGluLeu GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTG AspSerSerLeuLeuPheSerGluAlaAlaThrGlyGluGluSerLeuLeuSerGluGly	241 LeuargGluSerLeuSerPheTyrIleSerLeuAsnassganicIIIC.c.m.igasgasgasgasgasgasgasgasgasgasgasgasgasg	RESULT 3 AX511153 LOCUS LOCUS DEFINITION Sequence 4 from Patent W00242452. DEFINITION SACIDSSION AX511153 VERSION AX511153 Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (hordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.	and Loreto,M.P. 10- 10- 10- 10- 11- 11- 11- 11- 11- 11	Alignment Scores: Pred. No.: Pred. No.: 1347.00 Matches: Score: Percent Similarity: 99.62\$ Mismatches: 1

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1 Cases 1 to 786)

Loreto,M.P. and McGlade,C.J.

Direct Submission

Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for

Sick Children, 555 University Avenue, Toronto, Ont MSG 1X8, Canada

Location/Qualifiers
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1. (bases 1 to 786)

1. (bases 1 to 786)

1. (bases 1 to 786)

1. (bases 1 to 786)

1. (cloning and McGlade, C. J.

Cloning and characterization of human Src-like adaptor protein 2 and a novel splice isoform, SLAP-2-v

Oncogene 22 (2), 266-273 (2003)

12527895
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Query Match:
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AGGPAELSLRIGEPTITUSEDGDWWTVLSEVSGREYNIPSVHVAKVSHGMLYEGLSFP
AGGPAELSLRIGBFTITUSESGOTRAGSYSLSVRLGSRAPANDRIRHYRIHGLDNGGARE
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11 AND CHARLES AND	Location/Qualifiers 1. 786 / organism="Homo sapiens" / organism="Homo sapiens" / do xref="teaxon:9606" / chromosome="20" 1. 786 / note="SLAP2; SH2 and SH3 domain-containing adaptor" / codon_start=1 / product="src-like adapter protein-2" / product="src-like adapter protein-2" / product="src-like adapter protein-2" / product="src-like adapter protein-2" / product="src-like adapter protein-2" / do xref="do" 16798982" / do xref="do" 16798982" / do xref="do" 16798982" / do xref="do" 16798982" / do xref="do" 16798982" / do xref="do" 1679898888888888888888888888888888888888	<pre>nment Scores:</pre>	GINGLYGINGLYPROVALThrMetGluhla [ABOUT DE PROSEEVA HHISVALOLY EVALSETHISCHYTTHE ABOUT CCCCAGGGGTCCACGGGCCAAAGTCTCCCATGGGTGGAAAGTCTCCCATGGGTGGAAAGTCTCCCATGGGTGGAAAGTCTCCCATGGGTGGAAAGTCTCCCATGGGTGGAAAGTGGTGTTACTTAC
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Homo sapiens Src-like-adaptor 2, transcript variant 1, mRNA (cDNA clone MGC:49845 IMAGE:4429896), complete cds.

BC042041 GI:27469847
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SPRLTFPSLQALVDHYSELADDICCLIKEPCVLQRAGPLPGKDIPLPVTVQRTPFLNWK
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Shibahara, T. Tanaka, T. and Nakamura, Y.

Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-549-546, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Fax:81-3-549-5416, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Fax:81-3-549-5416, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Fax:81-3-549-5416, Shirokane-dai, Association for Superchalogy, cDNA full insert sequencing: Research Association for Blotechnology, cDNA library construction, S'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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OkamCo,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
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AspSerSerLeuLeuPheSerGluAlaAlaThrGlyGluGluSerLeuLeuSerGluGly
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Best Local Similarity:
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AK025645
LOCUS
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ORGANISM
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TITLE JOURNAL REFERENCE AUTHORS

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

source

FEATURES

CDS

Pred. No.: Score:

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540 180

160

100 360 120 420

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80

240

9

180 40

200 999 220 720 240 780 260 840

900

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	AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shamen, C.M., Schuler, G.D., Alteschul, S.F., Zeeberg, B., Buercow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diarchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P.P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Gonsak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulk, S.W., Kullalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A. Whiting, M., Madan, A., Roung, A. C., Shevchenko, Y., Banchez, A. Whiting, M., Madan, A., Koung, A. C., Shevchenko, Y., Banchez, A. Whiting, M., Madan, A., Koung, A. C., Shevchenko, Y., Banchez, A. Whiting, M., Madan, A., Koung, A. C., Shevchenko, Y.,	Dickson, M.C., Radariguez, A.C., Grimmond, J., Grimutz, J., Myers, R.M., Dickson, M.C., Raddriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schorerch, A., Schein, J.E., Gones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences MEDLINE 22388257 PUDMNED Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	REFERENCE 2 (bases 1 to 2538) AUTHORS Strausberg, R. TITLE Direct Submission JOURNAL Submitted (32.PEC-2002) National Institutes of Health, Mammalian JOURNAL Submitted (32.PEC-2002) National Office, National Cancer Institute, 31 Center Drive, Room 11803, Bethesda, MD 20892-2590, USA REMARK NIH-MGC Project IRT. http://mcc.nci.nih.gov	Contact: MGC help desk Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: (Dickson, Mark) mcd@paxil.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	Clone distribution: MGC clone distribution information can be found through the I.M. AG.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 88 Row: a Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422. FEATURES 1. 2538 Organism="Homo sapiens" AD.Lype="MRNA" A	/lab_host="DH10B"	/db_xref="LocusID:84174" /db_xref="MIM:606577" 3631148 /codon_start=1 /produce="Src-like-adaptor 2, isoform a" /produce="Src-like-adaptor 1, isoform a" /produce="Src-like-adaptor 1, isoform a" /produce="Src-like-adaptor 2, isoform a" /db_xref="G1:27469843" /db_xref="G1:27469843" /db_xref="LocusID:84174" /db_xref="G1:27469843" /db_xref="LocusID:84174" /db_xref="RocusID:84174" /db_xref="Locus

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161 SerProArgLeuthr PheProSerIeuGlaAlaleuvalAspHisTyrserGluleuAla 180 161 SerProArgLeuthr PheProSerIeuGlaAlaleuvalAspHisTyrserGluleuAla 180 181 SerProArgLeuthr PheProSerIeuGlaAlaleuvalAspHisTyrserGluleuAla 180 181 AspAspIleCysCysLeuteuCrysCuroCysValLeuGlaArgTyrsCrysGcCGGCTGCCT 1014 181 AspAspIleCysCysLeuteuCrysGluProCysValLeuGlaArgAlaGlyProLeuPro 201 182 AspAspIleCysCysLeuteuProValTyleuGlaArgThrProLeuAspHisTyleu 200 181 AspAspIleCysCysCysLeuteuProValTyleuGlaArgThrProLeuAspHisTyleu 201 182 AspAspIleCysCysCysCysCysLeuteuProValTyleuGlaArgThrProLeuAspHisTyleu 201 183 AspAspIleCysCysCysCysCysCysCysCysCysTyleuGlaArgThrProLeuAspHisTyleu 201 184 AspAspIleCysCysCysCysCysCysCysCysTyleuGlaArgThrProLeuAspHisTyleu 201 185 AspAspIleCysCysCysCysCysCysCysTyleuGlaArgThrProLeuAspHisTyleu 201 186 AspAspIleCysCysCysCysCysCysCysCysCysCysCysCysCysC	REFERENCE TITLE TOURNAL Part (DECEMBER) ONGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. REFERENCE 1 Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S., Dugas, M., Eils, R., Brors, B. and Mergenthaler, S. TITLE TOURNAL Partent: WO 0303943-A 3014 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Dudwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten, PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE) FEATURES 1. 2788 // Acainsm="Homo sapiens" // Mol_type="unassigned DNA" // Ab_xref="taxon:9606"	Alignment Scores:
DD 1083 CTCCGGAGTCCCTCAGCTTCTACATCAGCTGAATGACGAGGCTGTTTTGAATGATGAT 1142 QY 261 Ala 261 DD 1143 GCC 1145 RESULT 9 AX452880 LOCUS LOCUS AX452880 AX45280 AX45280 AX4570a AX462A17AR AMMANIA ARAACA AMMANIA ARAACA AMMANIA ARAACA AMMANIA ARAACA AMMANIA ARAACAA AMMANIA ARAACAA AMMANIA ARAACAA AMMANIA ARAACAA AMMANIA ARAACAAA AMMANIA ARAACAAA AMMANIA ARAACAAA AMMANIA ARAACAAAA AMMANIA ARAACAAAA AMMANIA ARAACAAAA AMMANIA ARAACAAAA AMMANIA ARAACAAAAA AMMANIA ARAACAAAAAA AMMANIA ARAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Alignment Scores: 1.55e-101 Length: 2567	QY 41 Gly8erPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThr 60 Db 535 GGCAGTTTCCGGCAGCTGCGCTGAGCTCGGGGGGCCATTGCC 594 QY 61 IleValSerGluAspGTrpTrpTrvalLeuSerGluValSerGlyArgGluTyr 80 Db 595 ATCGTCTCTGAGATGGAGACTGGTGGACGTGCTGTCTGAAGTCTCAGGCAGAGTAT 654 QY 81 AsnIleProSerValHisValGlyLysValSerHisGlyTrpTreuTyrGluGlyLeuSer 100 Db 655 AACATCCCCACGTCACAGGACGAAGTCTCCCAAGGTCTAGAGGTCTAGAGGTCTATAGAGGCTGTAGGGCTGTAGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGCTGTAGGGGGCTTAGGGGGCTTAGGGGGGCTTAGGGGGGCTTAGGGGGGCTTAGGGGGGGG

Query Match: 88.43* Indels: 19 DB: 6 Gaps: 1 US-09-939-853A-75 (1-261) x AX511155 (1-737)	Oy 1 MetGlySerLeuProSerArgArgLysSerLeuProSerProSerLeuSerSerVal 20	Qy 21 GlnGlyGlnGlyProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeu 40	Oy 41 GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluBroLeuThr 60	Qy 61 IleValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr 80	Qy 81 AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100	Oy 101 ArgGluLysAlaGluGluLeuLeuLeuLeubroGlyAsnProGlyGlyAlaPheLeulle 120	Oy 121 ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla 140	Qy 141 SerTrpAspArgIleArgHisTyrArgIleHisCysLeuAspAsnGlyTrpLeuTyrIle 160 L	Oy 161 SerProArgleuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla 180	Qy 181 AspAspIleCysCysLeuLysGluProCysValLeuGln-ArgAlaGlyProLeuPr 200	Qy 200 oGlyLysAsp11eProLeuProValThrValGlnArgThrProLeuAsmTrpLysGluLe 220	240 YLeuArgGluSer 	260 spala 261 730 Ardcc 734	RESULT 12 AF290986 LOCUS AF290986 DEFINITION Home sapiens Src-like adaptor protein-2 splice isoform mRNA,	322	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OY 61 IleValSerGluAspGlyAspTrpThrValLeuSerGluValSerGlyArgGluTyr 80	Oy 81 AsnIleProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100 	Oy 101 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyAlaPheLeulle 120	Qy 121 ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla 140	Oy 141 SerTrpAspArgIleArgHisTyrArgIleHisCysLeuAspAsnGlyTrpLeuTyrIle 160	Oy 161 SerProArgleuThrPheProSerLeuGlnAlaleuValAspHisTyrSerGluLeuAla 180	Qy 181 AspAspIleCysCysLeuLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro 200	Qy 201 GlyLysAspileProLeuProValThrValGlnArgThrProLeuAsnTrpLysGluLeu 220	Qy 221 AspSerSerLeuLeuPheSerGluAlaAlaThrGlyGluGluSerLeuLeuSerGluGly 240	Qy 241 LeuArgGluSerLeuSerPheTyrIleSerLeuAspAspGluAlaValSerLeuAspAsp 260	Qy 261 Ala 261 Db 1167 GCC 1169	RESULT 11 AX511155 AX511155 AX511155 DOCUS DEFINITION Sequence 6 from Patent W00242452. ACCESSION AX511155 REVENOR AX511155.1 GI:23392047	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryotes, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Euteleostomi;	reto, M.P.	ਜ਼ ਰੋਹ=	Scores:	

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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Sequence 2 from Patent W00242452.
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                                                                                                                                                 [Doreto, M.P. and McGlade, C.J.]

Loreto, M.P. and McGlade, C.J.

Direct Submission

Submitted (2011-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont MSG 1X8, Canada Location/Qualifiers
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                              Loreto, M.P. and McGlade, C.J.
Cloning and characterization of human Src-like adaptor protein
and a novel splice isoform, SLAP-2-v
Oncogene 22 (2), 266-273 (2003)
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        to 737)
and McGlade, C.J.
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note="SLAP-2-v"
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AF287467 1348 bp mRNA linear ROD 03-JUN-2002 Mus musculus Src-like adaptor protein-2 mRNA, complete cds. AF287467
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;

Mus.

Loases 1 to 1348)

Loreto,M.P., Berry,D.M. and McGlade,C.J.

Punctional cooperation between c-Cbl and Src-like adaptor protein in the negative regulation of T-cell receptor signaling

Mol. Cell. Biol. 22 (12), 4241-4255 (2002)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Adapter gene
Patent: WO 024252-A 1 30-MAY-2002;
The Hospital for Sick Children (CA)
Location/Qualifiers
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Sequence 1 from Patent W00242452.
AX511150
AX511150.1 GI:23392044
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Mus musculus
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LDRSLLFLEAPASGEASLLSSGLRESLSSYISLAEDPLDDA
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            Loreto, M. P. and McGlade, C.J.
Loreto, M. P. and McGlade, C.J.
Loreto, M. P. and McGlade, C.J.
Submitted (14-UUL-2000) Brain Tumour Research Centre, Hospital for Sick Children, 555 University Avenue, Toronto, Ont MSG 1X8, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 CCAGACCAGGAACCCGTGTCCATGCAACCAGAAAAGAACAAAGGTCACAGCTGTGGCCCTG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer
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                                                                                                                                                                                                                                codon_start=1
product="Src-like_adaptor_protein-2"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                         1. .1348 / Organism="Mus musculus" / mol type="mRNA" / db_xref="taxon:10090" / dev_stage="day 15 embryo" / 282. .1061
                                                                                                                                                                                                                                                                                                                                                                                                                     381. .551
/note="Region: SH3 domain"
                                                                                                                                                                                                                                                                    protein_id="AAL38196.1"
db_xref="G1:17351919"
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                                           181 AspAspIleCysCysLeuLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro
                                                              221 AspSerSerLeuLeuPheSerGluAla --- AlaThrGlyGluGluSerLeuLeuSerGlu
                                                                                                201 GlyLysAspIleProLeuProValThrValGlnArgThrProLeuAsnTrpLysGluLeu
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                                                                                                                                                                                                                RESULT 1
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-MODEL=frame+ pan.model -DBV=xlp
-MODEL=frame+ pan.model -DBV=xlp
-G=CGDZ_1/USFTO_spool_p/US0993983/runat_19022004_145338_24420/app_query.fasta_1.455
-DB=N_Geneseq_29Gan04 -OFMN=fastap_SUPFIX=p2n.rng
-MNDMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MINS -D -ALIGN=15
-MODE=LOCAL -OUTPMT=pco -NORM=ext -HEAPSIZE=500 -MINIENE0 -MAXIEN=200000000
-USRE-USO9939853 @CGN 1 1 708 @runat 19022004 145338 24420 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG-SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=10 -WARN TIMBOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOR=6
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1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA
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5.1.6
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                                                                                                                                                             2004, 09:33:07;
  GenCore version
Copyright (c) 1993 - 2004
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ALIGNMENTS

(CORT-) COR THERAPEUTICS INC

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polypeptides for treating or preventing a disorder associated with n, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.
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            Grosse WM, Hart M, Kekuda R, Shimkets RA; Tomlinson JE, Topper JN, Yang R;
                                                                                                                                                                                                                                                                                                                                US-09-939-853A-75 (1-261) x ABK61465 (1-1183)
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              Grosse WM,
                                                                           Claim 1; Page 98; 263pp; English.
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             Conley PB,
Szekeres ES,
            Conley
                                 WPI; 2002-280937/32
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Best Local Similarity:
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              Burgess CE,
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임 à 엄 Op Dp ò 셤 à δ 원 ò ٠.-The invention relates to an isolated polypeptide (NoVX) a mature form of NoVX, a NoVX variant (differing by no more than 15%), the nucleotide concoling NoVX (or its complement, fragment or variant). NoVX is NoV1-14, 154, 15b, 16a, and 16b. The NoVX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NoVX-associated disorder in humans, e.g. cardiomyopathy, atheroscierosis, a disorder related to cell signal processing and metabolic pathway modulation, diabetes or cancers. The NoVX polypeptide are metabolic pathway modulation, diabetes or cancers. The NoVX polypeptide or predisposition to the diseases. The NoVX nucleic acid and polypeptide are specially useful in therapeutic or prophylactic applications for cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus or sociated with aberrant NoVX expression or activity, e.g. cancers; immunodeficiency syndrome (AIDS), asthma, crohn's disease, hypertension, congenital heart defects, multiple scleroais, inflammation or Albright preditary osteodystrophy and many other diseases listed in the conditions. The DNA encoding the protein is useful in denethon assays, or the charting the conditions. This is also useful in detection assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present constitutions in the present constitutions. The DNA protein diagnostic applications or proprious applications or human disorders, as well as in diagnostic applications. The present constitutions or functional analysis of various constitutions and the defense and developing the defense and developed and developed and devel 120 100 697 757 517 577 637 457 80 40 9 20 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIle GGCAGTTTCCCGGCCAGGTGGCCCGGCCGAGCTGTCGCTGAGACTCGGGGAGCCATTGACC IleValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr Arcercrereaeeareeaecreereeaeereerererereaeaereeaeeaerer AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer GlnGlyGlnGlyProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeu GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThr MetGlySerLeuProSerArgArgLysSerLeuProSerProSerLeuSerSerVal Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 U; 0 Other; 1183 261 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:

1177 1057 1117 220 240 180 200 997 140 160 937 817 877 gene therapy; modulator of antigen receptor signalling; Human modulator of antigen receptor signalling protein coding sequence. GCCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTG TOACCGCGCCTCACCTTCCCCTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCG LeuArgGluSerLeuSerPheTyrIleSerLeuAsnAspGluAlaValSerLeuAspAsp 1118 CTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGATGACGAGGCTGTCTCTTTGGATGAT Human, gene, ss, genë therapy, modulator of antigen receptor signallin MARS, tumour suppressor gene, Scr-like adaptor protein, SLAP, mayeloid malignancy, acute myelogenous leukaemia, autoimmune disorder, immunosuppression, myeloproliferative disorder, breast cancer. ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla SerTrpAspArgIleArgHisTyrArgIleHisCysLeuAspAsnGlyTrpLeuTyrIle SerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla AspAspIleCysCysLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro GATGACATCTGCTGCCTACTCAAGGAGCCCTGTGCTCCTGCAGGGGCTGGCCGCCCCCT GlyLysAspileProLeuProValThrValGlnArgThrProLeuAsnTrpLysGluLeu 1058 GACAGCICCCICCIGITITCIGAAGCIGCCACAGGGGAGGAGCICTICTICAGTGAGGGI AspSerSerLeuLeuPheSerGluAlaAlaThrGlyGluGluSerLeuLeuSerGluGly ceesagaeccaeaccaesagaeccaecternactererereresecceeceresea New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders. "Human MARS protein" location/Qualifiers (HOSP-) HOSPITAL FOR SICK CHILDREN ВР. AAL44089 standard; cDNA; 786 26-NOV-2001; 2001WO-CA001662 27-NOV-2000; 2000CA-02324663 /*tag= a /product= " (first entry) Mcglade JC, Loreto MP; WPI; 2002-566564/60. 1180 P-PSDB; AAO15457 261 Ala 261 WO200242452-A2 D C C Homo sapiens 03-OCT-2002 30-MAY-2002 878 201 241 121 758 141 161 181 938 221 1178 AAL44089 g a à ò 원

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                                    The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Scr-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myelogenous leukaemia) autoimmune malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a human MARS protein
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The present sequence encodes the human Src-like inhibitory molecule (SLIM) protein (I). The present invention describes a SLIM protein comprising an N-terminal myristylation sequence, an N-terminal SH3 domain which can bind to Cbl, or comprising an N-terminal SH3 domain which can bind to Cbl, or comprising an N-terminal myristylation sequence and an N-terminal SH2 domain which is unable to bind to Cbl. (I) has antiinflammatory, immunosuppressive and anti-HTV activities, and can be used as a modulator of lymphocyte activation, and of ubiquitination of a Cbl target protein, and in gene therapy. (I) is useful for screening a bioactive agent capable of binding the SIM N standard or in the streament of conditions which involves this function or
CTCCGGGAGTCCCTCGACTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGAT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLAP; inhibitor; antiinflammatory; immunosuppressive; anti-HĪV; modulator; lymphocyte; CDi, gene therapy; immunodeficiency disorder; acquired immune deficiency.syndrome; AIDS; acute inflammatory disorder; chronic inflammatory disorder; autoimmune disorder; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the treatment of conditions which involves this function or dysregulation of SLIM protein activity, i.e. to diagnose, treat or prevent SLIM associated disorders. (I) or the polynucleotide encoding it (II) is useful for modulating leukocyte and/or platelet activation, for modulating antigen receptor-induced signalling and activation in leukocyte and/or platelets and for modulating antigen receptor-induced signalling and activation in lymphocytes and/or mast cells. (I) or (II) is also useful for modulating the basal activity of lymphocytes. (I) or (II) or (II) or (II) and outside the pasal activity of lymphocytes. (I) or (II) or (II) or (II) and (II) or (II) or (II) and (II) or (II) or (II) or (II) and (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (II) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (III) or (IIII) or (III) or (III) or (III) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIII) or (IIIII) or (IIII) or (IIII) or (IIII) or (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Src-like inhibitory molecule; SLIM; Src-like adapter protein;
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Sheng N;
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Shen M, Liao XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Src-like inhibitory molecule (SLIM) encoding cDNA.
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product= "SLIM"
/note= "Src-like inhibitory molecule"
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(II) is useful in the treatment of immunodeficiency disorders, such as acquired immunodeficiency syndrome (AIDS), for the prevention and treatment of acute inflammatory disorders, chronic inflammatory disorders, autoimmune disorder and transplant rejection
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The invention relates to a substantially purified human SH2/SH3-domain-
containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-
containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-
COT I invention is useful for treating an immune disorder involving
the invention is useful for treating or inhibitors of the invention is
cuseful for screening for antagonists or inhibitors of the invention of
the SLAP-2 with cellular signalling compounds, for diagnosting, treating or
preventing diseases or disorders associated with aberrant or uncontrolled
collular signal transduction, for determining those cellular signalling
molecules which associate with hSLAP-2 and which provide critical signals
collular signal transduction, for determining those cellular signalling
collular signal transduction; for determining those cellular signals
collular signal transduction is useful in screening assays to identity and
detect candidate bioactive agents that modulate hSLAP-2 bioactivity, for
corditional use to treat autoimmune diseases which may be caused by
hyperactivated B cells, as well as to treat diseases which may be caused
by hyperactivated C cells, in addition to other immune system related
conditions, diseases, or diseases, and conditions, rheumatoid arthritis,
conditions, diseases, or diseases and conditions, rheumatory bowel disease (Crohn's
conditions, diseases, and conditions, rheumatory disease (Crohn's
maxt cells or eosinophils, autoimmune diseases such as systemic lupus
cychematorus and multiple solerosis, pulmonary diseases including
cathma, acute respiratory distress syndrome, and chronic obstructive
collinant disorder, tissue/ organ rejection and cancer. The invention is
cuseful in gene therapy. The present sequence is human SLAP-2 conA
                                                                                                                                                                                                                                         SLAP-2, immune disorder; signal transduction, autoimmune disease, cancer; neoplasm; inflammation disorder; rheumatoid arthritis; osteoarthritis; postrasis; rhinitis; allergy; inflammatory bowel disease; gene therapy; Crohn's disease; systemic lupus erythematosus; tissue/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic intervention in immunological and inflammatory disorders and cancer.
                                                                                                                                                                                                                      SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2;
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                                                                                                                                                                         Human Src-Like Adapter Protein-2 (hSLAP-2) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human SLAP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GS,
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                                               AAD43980 standard; cDNA; 2567
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                                                                                          AAD43980;
RESULT 4
AAD43980
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(first entry)

08-FEB-2001

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GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGACACCACTCAACTGGAAAGAGCTG 1074
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             Length:
Matches:
Conservative:
Mismatches:
Indels:
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               2.19e-108
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Alignment Scores:
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Whuman, open reading frame, ORFX, detection; cytostatic; hepatotropic; wulnerary; antipsoriatic; antiparkinsonian; nootropic, neuroprotective; wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antiborouslant; osteopathic; antiantitic; immunosuppressate; cardiant; with immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; whypotensive; dermatological; immunosuppressive; antidiabetic; antibarcerial; antifungal; antiinfammatory; antidiamal control antibarcerial; antifungal; antidiamatory; which antidiamed control sent therapy; cancer; proliferative disorder; hypothyroid; who artically antidiamed antidiamed control ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; wound; whome damage; cartilage damage; antidifiammatory disease; coagulation; thrombosis; contraceptive; ss.
                        Human ORFX ORF2757 polynucleotide sequence SEQ ID NO:5513
                                                                                                                                                                                                                                                                                                                                          31-MAR-1999; 99US-0127607P.
02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US008621
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Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease. WPI; 2000-602362/57. P-PSDB; AAB42993.

Shimkets RA, Leach M;

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Claim 5; Page 4692-4693; 5507pp; English

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic, hepatotropic, vulnerary; antiparial antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporvalsant; antiparkinsonian; nootropic; antidabetic; hypotensive; dermatological; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antibacterial; antivingal; antithewmatic; antithyroid; and antianaemic. The antiviral; antithugal; antithewmatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OKFX-associated disorder. The nucleic acids can be used to express OKFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft ve host disease, cardiovascular disease, disorders, osteoarthritis, graft ve host disease, cardiovascular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartiage damage, nocturnal haemoglobinic, and antinifamment to coagulation; to inhibit thrombosis; and as a contraceptive enhance

Seguence 837 BP; 176 A; 254 C; 245 G; 160 T; 0 U; 2 Other;

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837
244
1
                 Matches:
Conservative:
Mismatches:
        Length:
       3.67e-102
1269.00
99.19%
98.79%
                           Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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AAC77202 standard; cDNA; 837 BP

AAC77202

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Human, expressed sequence tag, EST, chromosome 20, haematopoietic disorder, central nervous system disease, viral infection, peripheral nervous system disease, non-healing wound; infectious disease, immune disorder, bacterial infection; allergy; cancer, fungal infection; autoimmune disorder; coaquiation disorder, notropic; antiallergic; autiinflammatory; immunosuppressive; neuroprotective;
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The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polynuclectides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed sequence tags (STTS) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expensive of bio-pharmaceuticals or the development of plusplantation, and explained to research for re-engineering damaged or ties development of bio-sensors. The useful for re-engineering damaged or the development of bio-sensors. The polynucleotides and proteins are useful for preventing; treating or ampliorating disorders involving aberrant protein expression or biological activity. e.g. haematopoietic disorders, central/peripheral cor thunds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic contral, bacterial or fungal infection, autoimmune disorders, allergic polynucleotide sequences of the invention were assembled from BCTS isolated mainly by sequencing by hybridisation, and in some cases, care after this patent did not form part of the printed specification, but the printed specification, but were obtained in electronic format directly from VIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 CAAGGCCAGGGACCTGTGACCATGGAAGCAGAGAAGCAAGGCCACAGAGGCGTGGCCTG
                                                                                                                                                                                                                                                                                                                            Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 Aricecacerciacecacacacacacacacacececeasececaacerraserrecretee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                              Zhang J,
cytostatic, haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective; gene therapy; gene; ss.
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Wehrman T, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 107; 394pp; English
                                                                                                                                                                                             16-NOV-2001; 2001WO-US042950.
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us-09-939-853a-75.p2n.rng

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modulator
                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of modulato of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Scr-like adaptor protein (Simb). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogenous leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a mouse MARS protein.
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                                                                                                                                                                                                          New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders.
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                                                                        IlevalSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr
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                                                                                                                                      AsnIleProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer
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23-AUG-2000; 2000US-00649167.
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involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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1634 GGGCTCCGGGAGTCCCCTCAGCTTCTACATCAGCCCTGAATGACGAGGCTGTCTTTTG 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of modulator of antigen receptor signalling (MARS) proteins. The MARS protein is a putative tumour suppressor gene and exhibits structural and sequence similarity to the Sor-like adaptor protein (SLAP). The MARS DNA and protein sequences of the invention are useful for the treatment of myeloid malignancies (e.g. acute myelogencus leukaemia) autoimmune disorders, immunosuppression, myeloproliferative disorders and malignancies related to the de-regulation of tyrosine kinases (e.g. breast cancer). The present cDNA sequence encodes a mouse MARS protein
                                                                                                                                                                                                              ss; gene therapy; modulator of antigen receptor signalling;
                                                                                                                                                                                   Mouse modulator of antigen receptor signalling protein coding sequence.
                                                                                                                                                                                                                         MARS; tumour suppressor gene; Scr-like adaptor protein; SLAP; myeloid malignancy; acute myelogenous leukaemia; autoimmune disorder; immunosuppression; myeloproliferative disorder; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated modulator of antigen receptor signaling protein or its fragment, useful for treating malignant disorders such as myeloid malignancies, autoimmune disorders and myeloproliferative disorders
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P-PSDB; AAO15456.
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Pred. No.:
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MetGlySerLeuProSerArgArgLysSerLeuProSerProSerLeuSerSerSerVal 20

US-09-939-853A-75 (1-261) x AAL44087 (1-1348)

Length: Matches: Conservative: Mismatches:

Indels:

Percent Similarity: Best Local Similarity: Query Match:

No.:

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999 GGGCTCCGAGAGTCCCTCAGTTCCTACATCAGCCTGAGGAGC-----CCCTTGGAT 1052
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                                                              399 GGCAGTITCCCAGCAGGTGAACAGGCCAGACTATCTCTGAGACTCGGGGAGCCGCTGACC
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21 GlnGlyGlnGlyProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeu
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ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyAlaPheLeulle 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100
                                                                                                                                                                                                                                                                                                        New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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826.00
99.37%
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MEHRABAN F.
CONLEY P B.
TOPPER J N.
LAW D.
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P-PSDB; ABP64107.
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Query Match:
DB:
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGNs primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving districtions and its binding partners are useful for generating antibodies against it, detecting or quantitating a polypoptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and the major and to produce other types of data and products dependent on DNA and aming a generate the sequences in the envisations are considered to the products dependent on DNA and and the products of the envisations of the products of the envisations of the envisations and to produce other types of data and products dependent on DNA and the major of the envisations of the envisations of the envisations of the envisations of the envisations of the envisations and the envisations of the envisations of the envisations and the envisations of the envisations and the envisations and the envisations and the envisations and products dependent on DNA and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisations and the envisati
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                                                                                                                                                                                                                                                              159
                                                                                         121 ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla
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586 AGGGAGAAAGCAGAGGAACTGCTGTTGTTACCTGGGAACCCTGGAGGGGCCTTCCTCATC
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG10561.
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Alignment Scores

585

405

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us-09-939-853a-75.p2n.rng

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30-MAY-2000; 2000US-0208427P
                     (LEAC/) LEACH M D.
(WEIR/) MEHRABAN F.
(CONL) CONLEY P B.
(TOPP/) TOPPER J N.
(LAWD/) LAW D.
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Query Match:
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                                                                                       Leach MD,
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                                                                                                  ArgGluTyrAsnIleProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGlu
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 603
151
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                             US-09-939-853A-75 (1-261) x AAS74748 (1-603)
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4.2e-55
731.00
82.45%
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The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and numcleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, blood coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPPCO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                            New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
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Matches:
Conservative:
Mismatches:
Indels:
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   Conley PB,
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586.00
100.00%
100.00%
43.31%
Mehraban F,
                                                        WPI; 2002-626554/67.
P-PSDB; ABP64588.
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CCCCTGCCCAACCCGGAGGGACTGGATAGCGACTTCCCTTGCCGTGCTAAGTGACTACCCG 1217
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                                                                                                           T cell; gene; ss; differential expression; T cell activation; antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy; allergy; cancer; graft versus host disease; infection; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the sequences of several cDNAs that are differentially expressed in activated T cells. The sequences of the invention may have antiallergic, cytostatic, immunosuppressive and antimicrobial activity and may be used in gene therapy. The invention also comprises a method for screening samples for differentially expressed genes and a method for detecting these cDNAs by hybridisation. The methods and compositions of the present invention are useful for diagnosing, treating, staging or monitoring treatment for allergy, cancer, chronic graft versus host disease, infectious and/or autoimmune disorders. The present sequence represents a CDNA of the invention that is differentially expressed in activated T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 AlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrIleValSerGlu 64
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                                                                             Human activated T cell cDNA #91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 180pp; English.
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488.00
57.20%
39.30%
36.07%
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PETERSON D P.
COCKS B G.
HAWKINS P R.
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Best Local Similarity:
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                                                           104
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                                                                                                                                                                                                                                                                                                                    ThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAlaAspAspIleCys 184
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84
                                                                                                                                              1278 GAAGGGGGCTGGTGGAAAGCTATTTCTCTTAGCACTGGTCGAGAGAGTTACATCCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GluGluSerLeuLeu
 65 AspGlyAspTrpThrValLeuSerGluValSerGlyArgGluTyrAsnIleProSer
                                                           ValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSerArgGluLysAla
                                                                                            1338 ATATGTGTGGCCAGAGTTTACCATGGCTGGCTGTTTGAGGGCCTGGGCAGAGACAAGGCC
                                                                                                                                                                                                                                                      145 IlearghisTyrargileHisCysLeuAspasnGlyTrpLeuTyrIleSerProArgLeu
                                                                                                                                                                                                                                                                                     1500 GTAAAGCAITACCGCAITTTCCGICTGCCCAACAACTGGTACTACAITTCCCCGAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banville SC;
Shah P, Chalup MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding molecule for disease detection and treatment, mddt14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1791 AGCTATGGCCTTCGAGAGGATTGCCTCTTACCTGTCCCTGACCAGTGAG 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1680 AGCTCACCTGTCACCTTGCGTCAGAAGACTGTGGACTGGAGGAGAGTGTCCAGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGluGlyLeuArgGluSerLeuSerPheTyrIleSerLeuAsnAspGlu 254
                                                                                                                                                                                                                       1458 ACCAAGAAAGGGTTTTACTCACTGTCGGTGAGACAAAGG------
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Rosen BH,
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Cohen HJ,
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Dufour GE,
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Bratcher SR,
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30-NOV-1999;
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The sequence represents the coding sequence of molecule for disease detection and treatment, mddt14, shown by computer analysis to be similar to Str homology domain family of proteins. The sequence may be used for somatic or germline gene therapy. Gene therapy may be performed to: (i) correct genetic deficiency such as in severe combined immunodeficiency syndrome associated with adenosine deaminase (ADA) deficiency, cystic fibrosis, thalassaemias, familial hypercholesterolaemia and heemophilia caused by factor VIII or factor IX deficiencies; (ii) express a conditional lethal gene product (such as in the case of cancers which result from unregulated cell proliferation); (iii) express a protein which affords protection against intracellular parasites (for example, human retroviruses such as HIV, hepatitis B or C, fungal parasites such as Educiate albicans and Paracoccidioides brasiliensis, and protezoal
     R, Roseberry AM;
Amshey S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as Candida albicans and Paracoccidioides brasiliensis, and protozoal parasites such as Plasmodinium falciparum and Trypanosoma brasiliensis
                                                                                                                                                      Purified disease treatment and detection molecule polynucleotides and polypeptides, useful for providing diagnostic assays and gene therapy
Jones AL, Yu JY, Greenawalt LB, Panzer SR,
Chen W, Liu TF, Yap PE, Stockdreher TK, Ams
                                                                                                                                                                                                                                Claim 1; Page 103-104; 113pp; English.
                                                                                                        WPI; 2001-258131/26.
Hillman JL,
Wright RJ,
                                                      Fong WT;
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Sequence 2109 BP; 545 A; 538 C; 562 G; 464 T; 0 U; 0 Other;

	24 448	44 508	64 568	84	107	124	14,	164 85(184 91(
2109 102 47 47 17 3	ProSerArgArgLysSerLeuProSerLeuSerSerSerValGlnGlyGln-Gl	YProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeuGlySerPhePr 	oblaglyglyProblagluLeuSerLeuArgLeuGlygluProLeuThrIleValSerGl 	uaspglyasptrptrpthrvalleusergluvalserglyargglutyrasnileProse	rValhisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSerArgGluLysAl :::	userg1 :: GAGTGA	nThrargarglySerTyrSerLeuSerValargLeuSerargProAlaSerTrpaspar ::::::	gllearghistyrargilehisCysbeuaspasnGlyTrpLeuTyrileSerProargle :::::::	uThrPheProSerLeuGlnAlaLeuvalAspHisTyrSerGluLeuAlaAspAspIleCy
Length: Matches: Conservative: Mismatches: Indels: Gaps: 9 (1-2109)	ProSerProSerLeuSer6 ::: GGAAACAGCATGAAATCC	uArgSerLysAlaThrAla ::: CTGGATAGCGACTTCCTTC	uSerLeuArgLeuGlyGlu GATATTCCGCCGAGGGGA	LeuserGluValserGly -:: TATTTCTCTTAGCACTGG	rHisGlyTrpLeuTyrGlu ccArGGCrGGCrGTTTGA	aGluGlubeubeubeubeupzoGlyasnProGlyGlyalaphebeulleargGl 	rLeuSerValArgLeuSe: ACTGTCGGTGAGA	gllearghistyrargilehiscysleuaspasnGlytrpleutyri :::::::	aleuvalasphistyrse. ::: .ccregreaaccactarrc
5.59e-33 487.00 547.75 7: 39.53 35.99 4 4 AAS02049	ArgArgLysSerLeu :::::: AAAAAGAAAGAAATG	ThrMetGluAlaG 	YGlyProAlaGlube ::: TGACATCAGCCCCC	yaspirpirpihrva 	sValGlyLysValse ::: TGTGGCCAGAGTTTA	uLeuleuleuPr GCTGCTGCAGCTGCC	nThragargGlySerTyrSerLeuS : :::::: GACCAAGAAAGGGTTTTACTCACTGT	gHisTyrarglleHi :[GCATTACCGCATTTT	eProSerLeuGlnAl CAGTGCCTGGAGGA
t Scores: Similarity: al Similarit tch:	ന ര	24 yProva 449 CCCCTG	44 oAlaGl ::: 09 GTCTCC	64 uAspG1 ::: 69 TGAAGG	т О	104 aGluGl 689 CGAGGA	124 nThrAr : :: 749 GACCAA	144 gIleAr ::::: 791 GGTAAA	164 uThrPh 851 CACCTI
Alignment Sc Pred. No.: Score: Percent Simi Best Local & Query Match. DB:	88		ഗ	ľ	ب ب			•	
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911 CTGTGTGCTCACCACGCCCTGCCTGACACAAAGCACGGCTGCCCCAGCAGTGAGGGCCTC 970
                                                                                     224 uleuPheSerGluAlaAlaThrGly------GluGluSerLeuLe 237
sCysLeuLeuLysGluProCysValLeuGinArgAlaGlyProLeuProGlyLysAspIl 204
                                           204 eProLeuProValThrValGlnArgThrProLeuAsnTrpLysGluLeuAspSerSerLe 224
                                                                                                                                                                                                                                                                                         Human, cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                         971 CAGCTCACCTGTCACCTTGCGTCAGAAGACTGTGGAGGACTGGAGAGAGTGTCCAGA----
                                                                                                                                                1082 CAGCTATGGCCTTCGAGAGAGCATTGCCTCTTACCTGTCCCTGACCAGTGAG 1133
                                                                                                                                 237 uSerGluGlyLeuArgGluSerLeuSerPheTyrIleSerLeuAsnAspGlu 254
                                                                                                                                                                                                                                                                    Lung cancer related gene sequence SEQ ID NO:3526.
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2000US-0234923P.
2000US-0234924P.
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2000US-0234052P.
2000US-0234509P.
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02-OCT-2000; 2000US-0237294P
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2000US-0237295P

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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be bested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in certivity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which, is the data collected with respect to the anti-neoplastic agent. M1 can be used for producing a product which, is can anti-neoplastic agent. M1 can be used in the treatment of cancer such properties of the agent. M1 can be used in the treatment of cancer such concerns of the agent. M1 can be used in the treatment of cancer such properties of the agent. M1 can be used in the treatment of cancer such as cancer, such as cancer, infiltrating lobular cancer, squamous cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous the concerned on the treatment of cancer squamous the cancer infiltrating and Wilm's the cancer cancer.
                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                     Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3526; 44pp; English.
                                                                                                                                                                                                                                     Carter KC,
                                                        2000US-0237598P.
2000US-0237604P.
2000US-0237606P.
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2000US-0244867P.
2000US-0245084P.
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, Weaver Z;
                                                                                                                                                                                               (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                            WPI; 2002-188264/24.
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01-NOV-2000;
01-NOV-2000;
                  02-0CT-2000;
03-0CT-2000;
03-0CT-2000;
03-0CT-2000;
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Soppet DR,
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Sequence 2665 BP; 736 A; 617 C; 689 G; 623 T; 0 U; 0 Other; Alignment Scores:

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Score:	487.00	Matches:	101
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24	83	44	143	64	203	84	263	104	323
5 ProSerArgArgLysSerLeuProSerProSerLeuSerSerSerValGlnGlyGlnGly 24	GCATGAA	25 ProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeuGlySerPhePro 44	::: 84 CCCCTGCCCAACCCGGAGGGACTGGGATAGCGACTTCCTTGCCGTGCTAAGTGACTACCCG	45 AlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrIleValSerGlu 64	:::	S AspGlyAspTrpThrValLeuSerGluValSerGlyArgGluTyrAsnIleProSer 84	:::	85 ValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSerArgGluLysAla 104	HILLINITE HILL HILLINITE H
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GlugluLeuleuLeuLeuLeuproGlyAsnProGlyGlyAlaPheLeulleArgGluSerGln 324 GlugluLeuleuLeuLeuLeuproGlyAsnProGlyGlyAlaPheLeulleArgGluSerGln 324 GlugluLeuleuLeuCagacaCagaCag

Search completed: February 20, 2004, 09:56:47 Job time : 377 secs

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BQ052308 AGENCOURT
BQ052468 AGENCOURT
BQ052481 AGENCOURT
AXO88672 Mus muscu
AXO30877 Mus muscu
AXO20837 Mus muscu
BY742155 BY742155
AL641041 AL641041
BC054265 AGENCOURT
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AM59131 AL644311 AL644311
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AXO3665 Mus muscu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA 261
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Copyright (c) 1993 - 2004 Compugen Ltd.
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BQ052468
BQ052468.1 GI:19811808
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1 (bases 1 to 1069)
11. Mar. Mcc. nci.nin.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
clone through the I.M.A.G.E. Consortium/LLNL at:
plate: LLCM211B row: n column: 13
High quality sequence stop: 681.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       696 GGCAAGGATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                 AspSerSerLeuLeuPheSerGluAlaAlaThr-GlyGluGluSerLeuLeuSerGlu-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 GTCTCCGGGGAGTCCCTCAGCTTCTACATCAGCCCTGATGACGAGGCTGTCTCTTTGGA
                                                                                                                                                                                          181 AspAspIleCysCysLeuLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro
                                                                                                                                                                                                                                GATGACATCTGCTGCCTACTCAAGGAGCCCTGTGTCCTGCAGAGGGCTGGCCGCTCCCT
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                                                                                                             SerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla
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Homo sapiens
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                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Irissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM2118 row: d column: 23

High quality sequence stop: 670.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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S. Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Haramoto, K., Hiracka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Haramoto, K., Hiracka, T., Hirozane, T., Katoh, F., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kouda, M., Katoh, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Salto, R., Saltoh, H., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Saltoh, R., Sahai, C., Sakazume, N., Sano, H., Sasaki, P., Sahazume, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Direct Submission

L. Submitted (16-App-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegec:riken.go.jp,, Tel:81-45-503-9222, Prax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         con library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Mrc Dullding Addenbrookse Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://fantom.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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AEBLLLLEGRIPGGAPLIRESGTRRGCYSLSYRLERPSWWDR.THYRIQRLDNGWLYIS
PRLTPPSLHALVEHYSELADGICCPLREPGVLOKLGPLGFGFDPPPVTVPTSSLNWKK
LDRSTLFLERAPASGRASLLSEGERESISSYTSLAEDPDDDA"
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2637)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
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Standards. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Haramoto, K., Hiraoka, T., Hirozane, T., Haraja, M., Hiraoka, T., Hirozane, T., Haraja, M., Kadawa, T., Horai, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, J., Kojima, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, Y., Numazaki, R., Ohno, M., Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sarazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Taraka, T., Taraka, T., Taraka, M., Toya, T., Yasunishi, A., Takaku, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Dhysical and Chemical Research (RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; I.-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseges.riken.go.jp, URu, Itep://genome-ges.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 (111-length cDNAs Nature 420, 563-573 (2002)
6 (bases 1 to 2974)
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Rike
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK020837 1near HTC 20-SEP-2003 mRNA linear HTC 20-SEP-2003 Was musculus adult retina CDNA, RIKEN full-length enriched library, clone:A930009E21 product:MODULATOR OF ANTIGEN RECEPTOR SIGNALING MARS, full insert sequence.
                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hadama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watsahiki, M., Yonga, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunra, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 926)
829 GGCAAAGATACACCTCCACCTGTGACTGTGCCAACATCATCACTAAATTGGAAAAAGCTG 888
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                    AspSerSerLeuLeuPheSerGluAla---AlaThrGlyGluGluSerLeuLeuSerGlu
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Adachi,J., Alzawa,K. Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramcto,K.,
Hiracka,T., Hori,P., Imorani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H. Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y.; Okido,T., Owa,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA cloning
Wehl. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yagai, K., Tomaru, Y., Hasegawa, T., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C. Hume, D. A., Quackenbush, T., Blake, J. A., Bradi, D. Bult, C. Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragai, T. A., Fletcher, C. R., Frazer, K. S., Gaasterland, T. A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
                                                                                                                                                                                                             5 GCCAGTTTCCCAGCAGGTGAACAGGCCAGACTATCTCTGAGACTCGGGGAGCCGCTGACC
                                                                                                                                                                                                                                                                                                           121 ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla
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                                                                                                                                                                               61 lleValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr
                                                                                                                                                                                                                                                                             81 AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer
                                                                                                                                                                                                                                                                                                                                                                                 101 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                    185 CGGGAGAAAGCCGAGGAACTACTCCTGTTACCTGGGAACCCCGGAGGGGCCTTCCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 SerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AspAspIleCysCysLeuLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 GGCAAAGATACACCTCCCACCTGTGACTGTGCCAACATCATCACTAAATTGGAAAAAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 AspSerSerLeuLeuPheSerGluAla---AlaThrGlyGluGluSerLeuLeuSerGlu
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                                                                              41 GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 GATGGCATCTGCTGTCCCCTCAGGAGCCGTGTGTCCTGCAGAAGCTTGGGCCACTACCT
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                             US-09-939-853A-75 (1-261) x AK020837 (1-926)
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                                                                                                                                         AL SUBMILIED (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer (5' GAGAGAGAAGACTTTTTTTTTTTTTTTTVTV 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cape-trapper. CDNA went through two rounds of normalization to Rot = 20.0 and subtraction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; MODULATOR OF ANTIGEN RECEPTOR SIGNALING MARS (SPTR|AAL38196, evidence: FASTY, 100%ID, 100%length, match=777)
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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                   MEDLINE
PUBMED
COMMENT
              JOURNAL
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Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaj, H., Kawaswa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Naglott, D.R., Maltais, L., Marchioni, L., McKenzie, L., Miki, H., Nagachima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Pertrosky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Read, D., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Suttana, Y., Taylor, M.S., Tasdale, R.D., Tomita, M., Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Waranebe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Waranebe, Y., Verardo, R., Yang, L., Yang, Z., Zavolan, M., Simer, A., Carninici, P., Hayates, N., Hirozane-Kishikawa, T., Kommo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itch, M., Xagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Vokohama Institute The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical and Chemical Research (RIKEN) The Institute of Physical Research (RIKEN)

Email: genome_resegsc.riken.go.jp,

URL:http://genome_gsc.riken.go.jp,

Adachi,J., Aizawa.K., Akimura.T., Arakawa.T., Carninci,P.,

Pukuda.S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,

Imotani,K., Ishi,Y., Itoh,M., Kagawa,T., Kawai,J., Kojima,Y.,

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Nomura.K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,

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Direct Submission

Direct summissional Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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RIERN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

Feeins RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA Delis, USA) whose assistance is gratefully acknowledged.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details. prepare mouse tissues

location/Qualifiers

PEATURES

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645

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGACCTTTTTTTTTTTTVN 3'], cDNA was

ORIGIN

660 174 15 25 25 25 Matches: Conservative: Mismatches: Indels: 878.50 85.52% 78.73% 64.93% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: Pred. No.: Score:

(1-660)US-09-939-853A-75 (1-261) x BY742155

100 120 244 140 304 160 364 180 424 200 484 220 544 239 604 259 124 184 09 64 80 SerTrpAspArgileArgHisTyrArgileHisCysLeuAspAsnGlyTrpLeuTyrile GlyLysAspileProLeuProValThrValGlnArgThrProLeuAsnTrpLysGluLeu 5 edchérrircccháchádranachagáchancháricrcraháhartcsádáhachagáchánach 65 Arcarcricadadardedagarindericadardericadiodadagicricadedagadada 101 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIle AspAspileCysCysLeuLeuLysGluProCysValLeuGlnArgAlaGlyProLeuPro 545 gacceradecrecrerrirergandecacerecangedegedearerecrerrendad GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThr 81 AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer SerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAla 221 AspSerSerLeuLeuPheSerGluAla -- - AlaThrGlyGluGluSerLeuLeuSerGlu 61 IleValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr 121 ArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAla retradadecadadadacaeracadaaracaacarerraacaaradecraracare 365 141 305 161 181 201 Db g 임 ઠે 셤 ò 셤 셤 à ò 8 à g ò 원 à 임 ઠે g ₹ ò

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.
El (Dasses 1 to 566)
NIH-WGC http://mgc.nni.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMO418 row: c column: 07
High quality sequence stop: 566.
Location/Qualifiers
Location/Qualifiers
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/mol_type="mRMA"
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Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG284179 566 bp mRNA linear EST 21-FEB-2001 60240826F1 NIH_MGC_91 Homo sapiens cDNA clone IMACE:4520382 5', BG284179
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                                           81 AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100
639 ATCGTCTCTGAGGATGGAGACTGGTGGACGGTGCTGTCTGAAGTCTCAGGCAGAGAGTAT 698
                                                                                                                                    101 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIle
                                                                                                                                                            819 CGGGAGAGCCAGAMCAGGAGAGGCTCTTACTCTCTGTCAGTCCGCCTCAGCCGCCTGCA
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                                                                                                                                                                                                                         ArgGluSerGlnThrArgArgGlySerTyrSerbeuSerValArgbeuSerArgProAla
                                                                        161 SerProArgieuThrPheProSerLeuGlnAlaLeuValAspHisTyr 176
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E 1 (Bases 1 to 1201)

E 1 (Bases 1 to 1201)

E 11, W.B., Gruber.(C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

ID Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12871733.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
EMail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9825.r. For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.ggi?seq=cSODE005AF12QP1&cluster=9825.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
Location/Qualifiers
Location/Qualifiers
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/mol type="mRNA"
/db Xref="taxon:9606"
/clone="CSODEOSYX23"
/clone lib="Homo sapiens PlaCENTA"
/clone lib="Homo sapiens PlaCENTA"
/clone lib="Woctor: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                                     AL541041 Homo sapiens PLACENTA Homo sapiens cDNA clone CSCDE005YK23 5-PRIME, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Superscript II RT (Life Technologies). Note: this is NIH_MGC Library."
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BU944126.1 GI:24132945
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AGENCOURT 6830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936339
SQ054265.1 GI:19813605
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Upubblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2125 row: i column: 12
High quality sequence stop: 515.
                                                ThrArgArgGlySerTyrSerLeuSerValArgLeuSerArgProAlaSerTrpAspArg 144
                                                                                                                          164
                                                                                                                                                      ATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGCTGTACATCTCACGCGCGCCTC 123
                                                                                                                                                                                              ThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAlaAspAspIleCys 184
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 986)
                                                                                                                      145 ileArgHisTyrArglleHisCysLeuAspAsnGlyTrpLeuTyrlleSerProArgLeu
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                                                                                   4 Acadenceasacrerracrererandaresecreasecasecracarecrassas
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/clone_Torgan: blood; Vector: poTB7; Site_l: XhoI; Site_2:

/clone lib="NT Congress of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of taxons of
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AGENCOURT_6822017 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935253
BQ053486
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NH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2122 row: 1 column: 06
High quality sequence stop: 394.
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560.50
63.60%
58.77%
41.43%
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Homo sapiens
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TITLE
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BQ053486
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KEYWORDS
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                       1 (bases 1 to 960)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1049 row: m column: 21
High quality sequence stop: 628.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Matches:
Conservative:
Mismatches:
Indels:
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BB635615 RIKEN full-length enriched, 0 day neonate thymus Mus musculus cDNA clone A430076N07 5', mRNA sequence.
BB635615.1 GI:16471660
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Mammalia, Eutheriai, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Dases 1 to 660)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoco,K., Hori,F., Ishii,Y., Ito,M., Kawai,T.,
Konno,H., Kouda,M., Koya,S., Mastsuyama,T., Miyazaki,A., Nomra,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
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Conservative:
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         clone="IMAGE:1330042"
sex="male"
                                                            tissue type="Thymus"
dev stage="4 weeks"
lab host="DH10B"
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557.00
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                  101 ArgGluLysAlaGluGluLeuLeuLeuLeuLroGlyAsnProGlyAshApheLeuIle 120 :::||||||||||||||||:::
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                                                                                        AsnileProSerValHisValGlyLysValSerHisGlyTrpLeuTyrGluGlyLeuSer 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     723 CCCGGGACCC-----CCCTGGCCTTGACAATGGGGCTTGGGAAAATTTTT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashL-HMI Mouse EST Project
WashL-HMI Mouse EST Project
WashLngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:689586
513 AACATCCCCATCGTCCACGTGGCCAAAGTCTCCCATGCGTGGGCTGTATGAGGGCT--GAN
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377 bp mRNA linear EST 08-MAY.
VZSIQG6.r1 Soares_thymus_2NbMT mus musculus cDNA clone
IMAGE:1330042 5' similar to TR:013239 013239 PUTATIVE SRC-LIKE
ADAPTER PROTEIN ;, mRNA sequence.
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Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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The WashU-HHMI Mouse EST Project
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AA959151
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119 246 139

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67 79 306

357

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417

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477 100 537 120 597 140 657

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Email: hunguery@anger.ac.uk
Sangar Centre name: sccd100Hs.154136A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of CDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool of up to 100,000 cDNA clones derived from
thttp://www.sanger.ac.uk/Teams/Teams9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 30-JUL-2002
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 597)
Ashoroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapies BST sequence
Unpublished (2002)
Context: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA,
                                                                                                                                                                                                                                                        358 GGCAGTTTCCCAGCAGGTGAACAGGCCAGACTATCTCTGTAAGACTCGGGGAGCCGCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 ATCATCTCTGAGGATGGAGATTGGTGGTGGACAGTCCAGTCGGAAGTCTCAGGCAGAGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 cadababaccasadabactactactatracctangaaccocadagaccrrcctcatc
                                                                                                                                                                                                                                                                                                                                                             21 GlnGlyGlnGlyProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeu
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              118
       Mismatches:
Indels:
Gaps:
                                                                                                                                                    US-09-939-853A-75 (1-261) x BB635615 (1-660)
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              80.85%
41.13%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format Regenering pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome_res@gsc_riken.go.jp,
URL:http://genome.gsc_riken.go.jp,
URL:http://genome.gsc_riken.go.jp/
Carnindi.p. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper_selected cDNAs to
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Length: Matches: Conservative:

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215	215 LeuAsnTrpLygGluLeuAspSerSerLeuLeuPheSerGluAlaAlaAlaThrGlyGluGlu .234	234
193 (193 CTCAACTGGAAAGAGCTGGACAGCTCCCTCTTTTTTCTGAAGCTGCCACAGGGAGGG	252
235	235 SerbeuleuSerGluGlyLeuArgGluSerLeuSerPheTyrIleSerLeuAsnAspGlu 254	254
253	253 TCTCTTCTCAGTGAGGGTCTCCGGGAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAG 312	312

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SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS G.2
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FILING DATE: HEREWITH
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GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
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REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
\begin{array}{c} 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\ 276.5 \\
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cqg12_1/VBFPO spool_p/USO939833/runat_19022004_145340_24508/app_query.fasta_1.455
-Q=/Cqg12_1/VBFPO spool_p/USO939833/runat_19022004_145340_24508/app_query.fasta_1.455
-DB=ISSUGA_PATEPTO spool_p/USO939833/runat_1902.nrii_-MNMATCH=0.1_LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX b-losum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-LOCAL_-OUTFMT=Pto -NOGM=sxt -HARDS1ZB=500 -MINLEN=0 -MAXLEN=200000000
-USDR=USO939853 @CGN 1 1.85 @runat 19022004 145340_24508 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1105, Ap
Sequence 1452, Ap
Sequence 1313, Ap
Sequence 77, Appl
Sequence 77, Appl
Sequence 77, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1080, Ap
Sequence 2, Appli
                                                                                                                                                                                                                  2004, 09:40:13 ; Search time 89 Seconds (without alignments) 1627.440 Million cell updates/sec
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1 MGSLPSRRKSLPSPSLSSSV......RESLSFYISLNDEAVSLDDA
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11. \G972_6\Ptick_Ptodata/2/ina/5A_COMB.seq:*
12. \G972_6\Ptick_Ptodata/2/ina/5B_COMB.seq:*
31. \G972_6\Ptick_Ptodata/2/ina/6A_COMB.seq:*
41. \G972_6\Ptick_Ptodata/2/ina/6B_COMB.seq:*
42. \G972_6\Ptick_Ptodata/2/ina/FtoTUS_COMB.seq:*
43. \G972_6\Ptick_Ptodata/2/ina/PtoTUS_COMB.seq:*
44. \G972_6\Ptick_Ptodata/2/ina/PtoTUS_COMB.seq:*
45. \G972_6\Ptick_Ptodata/2/ina/PtoTUS_COMB.seq:*
46. \G972_6\Ptick_Ptodata/2/ina/PtoTUS_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                   OM protein - nucleic search, using frame_plus_p2n model
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US-09-023-655-1105
US-09-016-424-1452
US-09-220-1313
US-09-220-132-77
PCT-US93-06251-77
PCT-US93-06251-83
US-09-470-0881-7
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US-09-023-655-1080
US-09-470-881-2
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext (Ygapop 10.0, Ygapext (Ygapop 6.0, Fgapext Delop 6.0, Delext
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                     February 20,
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                           6 SerArgArgLysSerLeuProSerProSerLeuSerSerValGlnGlyGlnGlyPro 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeuGlySerPheProAla 45
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646 TATGTGGCCAAACTCAACACCTTAGAAACAGAAGAGGGTTTTTCAAGGATATAACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 TrpAspArgileArgHisTyrArgileHisCysLeuAspAsnGlyTrpLeuTyrileSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrIleValSerGluAsp
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                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 115-
SEQUENCE CHARACTERISTICS:
LENGTH: 2298 base pairs
                                                                                                                                                                                                                               9.15e-30
370.50
57.71%
39.80%
27.38%
                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                 CLONE: GENBANK
CLONE: 9187268
US-09-023-655-1158
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-023-655-1105
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Sequence 1105, Application US/09023655 Patent No. 6607879 GENERAL INFORMATION: APPLICANT: Cocks, Benjamin G.

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396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ProSerProSerLeuSerSerSerValGlnGlyGlnGlyProValThrMetGluAlaGlu 31
J. Seilhamer
COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 TCTGAGGACATCATCGTGGTTGCCTGTATGATTACGAGGCCATTCACCACGAAGACCTC
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                          TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COMPUTER: 9430 ds
ADDRESSE: Flopy disk
COMPUTER: FLOPSY disk
COMPUTER: FLOPSY disk
COMPUTER: FLOPSY disk
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-939-853A-75 (1-261) x US-09-023-655-1105 (1-2015)
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 cceeecciaaraeccacaacaec
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 11'
SEQUENCE CHARACTERISTICS:
LENGTH: 2015 base_pairs
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58.38%
41.62%
26.64%
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                 Jeffrey J.
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STRANDEDNESS: sing
Susan G.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: 9183911
US-09-023-655-1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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ery Match: 25.13\$ Indels: Gaps: -09-939-853A-75 (1-261) x US-09-016-434-1452 (1-2129) 26 ValThrMetGlualaGluargSerLysalaThr	DD 324 CGCATCCTGGAGCGGGGAGTGGTGGTGGCAGCGCAGTCCCTGACCACGGGCAA 383 Qy 80 TyrAsnIleProSerValHisValGlyLysValSerHisGlyTrpLeu 95	Oy 116 GlyAlaPheLeuIleArgGluSerGlnThrArgArgGlySerTyrSerLeuSerValArg 135	33 34 EV	Jeffrey NVENTION: NVENTION: SEQUENCES: ENCE ADDRI E: INCYTI 31.4 PORY ALO ALTO CALIFORNII USA 30.4 SAABLE FC	COMPUTER: IBM PC compatible COMPATION: PC-DOS/MS-DOS SOFTWARB: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,655 FILING DATE: HEREWITH CLASSIPICATION: PRIOR APPLICATION NUMBER: FILING APPLICATION NUMBER: CLASSIPICATION NUMBER: FILING DATE: APPLICATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION:
008 LeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIleArgGluSerGlnThrArgArg 127	Qy 188 LysGlubroCysVal 192 Db 817 TCGGTGCCTGCATG 831 RESULT 3 US-09-016-434-1452 ; Sequence 1452, Application US/09016434 ; Patent No. 6500938	HE HE CONTRACT	ZIF: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPARAZE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION NUMBER: US/09/016,434 FILING DATE: HEREWITH CLASSIPICATION: RRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION NUMBER:	CLASSIPLEATION: ATTORNEY/AGENT INPORMATION: NAME: Zeller, Karen J. REGISTATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0002 US TELECOMMUNICATION INFORMATION: TELEFANCE: (650) 845-4166 INFORMATION FOR SEQ ID NO: 1452: SEQUENCE CHARACTERISTICS: LENGTH: 2129 base pairs TYPE: nucleic acid	STRANDENESS: single

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Alignment Scores:
                                                                                                                                                                                                       LENGTH: 2647
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                                                                                                                                                                                          SEQ ID NO 77
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Matches:
Conservative:
Mismatches:
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                        US
                        PA-0001
         REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1313:
SEQUENCE CHARACTERISTICS:
LENGTH: 2435 base pairs
                                                                                                                                                                                                                                1.24e-24
323.00
51.74%
40.30%
23.87%
                                                                                                             TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIREARY: GENEANK

CLONE: 9338227

US-09-023-655-1313
Zeller, Karen J.
                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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US-09-220-132-77
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Patent No. 6506607

GENERAL INFORMATION:
ADDITIONAL AND ADDITION AND ASSESSMENT
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07344-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT APPLICATION NUMBER: US 60/079,303
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 191
NUMBER OF SEQ ID NOS: 191
NUMBER OF SEQ ID NOS: 191
NUMBER OF SEG ID NOS: 191
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Mismatches:
Indels:
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Sequence 77, Application US/09220132
Patent No. 6506607
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51.74%
39.80%
23.65%
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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1134

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Sequence 7, Application US/09470881

Patent No. 6655938

GRUBEAL INFORMATION:

APPLICANT: CHERESH, David A.

APPLICANT: ELICEIRI, Brian

TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF

TITLE OF INVENTION: AND TOGRENESS AND VASCULAR PERMEABILITY USING SRC OR

TITLE OF INVENTION: YES TYROSINE KINASES

FILE REPERBENCE: TSRI 651.2

CURRENT APPLICATION NUMBER: US/09/470,881

CURRENT FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-29

PRIOR FILING DATE: 1998-05-29
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GGAGCAGAACCCACTACAGTGTCACCATGTCCGTCATCTTCAGCAAAGGGAACAGCAGTT 363
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1015 GCAGAAGAGTACTTTGGAAAACTTGGCCGAAAAGATGCTGAGCGACAGCTATTGTCC
                                                                                                                                                                                                                                                151 HisCysLeuAspAsnGlyTrpLeuTyrIleSerProArgLeuThrPheProSerLeuGln
                                                                                                                                                                131 SerLeuSerValArgLeuSerArgProAlaSerTrpAspArgIleArgHisTyrArgIle
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                                                                                                              111 ProGlyAsnProGlyGlyAlaPheLeuIleArgGluSerGlnThrArgArgGlySerTyr
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113
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. OTHER INFORMATION: human Yes-1 cDNA translated protein
US-09-470-881-7
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Matches:
Conservative:
Mismatches:
Indels:
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315.50
43.22%
29.02%
23.32%
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENCTH: 4517
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Best Local Similarity:
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                                                                          Sequence 77, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 GGAGAAAATTTCAAATATTGAACAGCTCGGAAGGAGATTGGTGGGAAGCCCGCTCCTTG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GlyGluProLeuThrileVal---SerGluAspGlyAspTrpTrpThrValLeuSerGlu 74
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                                                                                                                                                                                                                                                                                                                        ZIP: 11330
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEFX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pairs
TYPE: nucleic acid
STRANDEDNESS: acubic
TYPE: nucleic acid
STRANDEDNESS: acubic
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320.00
51.74%
39.80%
23.65%
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Best Local Similarity:
TGT 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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1315
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DB:
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Patentin Release #1.0, Version #1.25
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TELEPRONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 4517 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/UG
FILING DATE: 19930630
CLASSIEFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIALO, FRANK S
REGISTRATION NUMBER: 31,34
REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                                                     TYPE: DNA (genomic)
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Query Match:
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PCT-US93-06251-83
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GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069 TTCGGCGAAGTGTGGAAGATGGAATGGAACCACGAAAGTAGCAATCAAAACACTA 1128
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 GGTGCATCTTCCTCATTTTCAGTGGTGCCAAGTTCATATCCTGCTGGTTTAACAGGTGGT
                                                              184 GTTACTATATTTGTGGCCTTATATGATTATGAAGCTAGAACTACAGAAGACTTTCATTT
                                                                                             54 ArgleuGlyGluProLeuThrileValSerGlu---AspGlyAspTrpThrValLeu
                                                                                                                           544 AAGAAGGSTGAAAGATTTCAAATAATTAACAATACGGAAGGAGATTGGTGGGAAGCAAGA
                                                                                                                                                                                       604 TCAATCGCTACAGGAAGAATGGTTATATCCCGAGCAATTATGTAGCGCCTGCAGATTCC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ArgleuGlyGluProLeuThrlleValSerGlu---AspGlyAspTrpTrpThrValLeu 72
                                                                                                                                                                                                                                                                                                                                                         ----GlnGlyGlnGlyProValThrMetGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GGTGCATCTTCCTCATTTTCAGTGCTGCCAAGTTCATATCCTGGTTTAACAGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 GITACTATATTTGTGGCCTTATATGATTATGAAGCTAGAACTACAGAAGACCTTTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 SerTyrSerLeuSerValArgLeuSerArgProAlaSerTrpAspArgileArg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 GluArgSerLysAlaThrAlaValAlaLeuGlySerPheProAlaGly----
4517
92
45
113
67
                                                                                                                                                                                         US-09-939-853A-75 (1-261) x PCT-US93-06251-83 (1-4517)
                                                       Conservative:
Mismatches:
Indels:
  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AAGAAAGÁGTCAGGGGAGTGGTGGGAAGCATGTCTAATTTCCACTGGTGAAGÁAGGCTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 TTCTTCATTTCTACACGGATCCCTTTTCCTTTGCCAGAGCTGGTACGCCATTATCAA 588
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APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF
TITLE OF INVENTION: USE THEREOF
WUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
         Conservative:
Mismatches:
Indels:
                                                                                                                                                            US-09-939-853A-75 (1-261) x US-09-006-675-1 (1-1491)
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411 Hackensack Avenue, 4th Floor
                                                                                                     Gaps:
                                                                                                                                                                                                                       MetGlySerLeuProSerArg-----
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      52.34%
36.45%
23.17%
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USA
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   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                      949 İĞCCACAAGİİĞACAACIGIĞİÇÇCAACIGIGAAACCICAGACICAAGGICIAGCAAAA 1008
                                                                                                                                                                                                                                                           .069 TTCGGCGAAGTGTGGATGGAACATGGAATGGAACCACGAAAGTAGCAATCAAAACACTA 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1129 AAACCAGGTACAATGATGCCAGAAGCTTTCCTTCAAGAAGCTCAGATAATGAAAAAATTA 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AspSerSerLeuLeuPheSerGluAlaAlaThrGlyGluGluSerLeuLeuSerGluGly 240
                                                                                              .-----ValLeuGln 194
889 GCACAATTTGATACTCTGCAGAAATTGGTGAAAACACTACACAGAACACTGCTGATGCTTA
                                                                                                                                                                                                                                                                                                                                            --ThrProLeuAsnTrpLysGluLeu
                                                                                                                                                                                                                    195 ArgAlaGlyProLeuProGlyLysAspileProLeuProValThrValGlnArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 LeuArgGluSerLeu---SerPheTyrIleSerLeuAsnAspGluAlaVal 256
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APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF
TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
                                                                                              184 CysCysLeuLysGluProCys-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09006675 Patent No. 5952213
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-
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313.50
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201-343-1684
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nucleic acid
EDNESS: double
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
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                                                                                                                                                                                                                                                                                                                                         213 ----
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, LOCATION:
US-09-006-675-1
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Pred. No.:
Score:
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529 ITCTICALITICIACACGGAICCCTITICCTICITIGCCAGAGCIGGIACGCCATIAICAA 588
                                         178 GluLeuAlaAspAspIleCysCysLeuLeuLysGluProCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: 9182573
US-09-023-655-1080
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STRANDEDNESS:
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US-09-023-655-1080
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Pred. No.:
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301 GITCCCAGTAACTAIGTAGCGTAITICAAITCCCIGGAAGAATCTGAAGAGTGGTACTITAAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AAGAAAGAGTCAGGGGAGTGGTGGAAGCATGTCTAATTTCCACTGGTGAAGAAGGCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyLeuSerArgGluLysAlaGluGluLeuLeuLeuLeuFroGlyAsnProGlyGlyAla 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------LysAlaThrAlaValAlaLeuGly 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SerHisGlyTrpLeuTyrGlu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ValThrMet----GluAlaGlu 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrIle 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyrAsn 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GACTCAGGGGACACTGTGAAACATTACAAAATTCGCACACTCGATGATGGAGGT
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-939-853A-75 (1-261) x US-09-228-603A-1 (1-1491)
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                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ArgSer-----
                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER ESTICS:
LENGTH: 1491 base pairs
                                 12-JAN-1999
                               FILING DATE: 12-JAN-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.34%
36.45%
23.17%
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lines
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-228-603A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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253 cérgaccccacradageccegecérecarecretarrecceaearecceaerracageaac 312
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                                                                                                                                                                                                                                                                  THE DETECTION OF BLOOD CELL GENE
630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ProSerArgArgLysSerLeuProSerProSerLeuSerSer--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
589 GGTAAAGTGGATGGCTTGTGTCAGTGCCTTACAATACCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-939-853A-75 (1-261) x US-09-023-655-1080 (1-2354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                      3: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                     FOR
                                                                                                Sequence 1080, Application US/09023655
Patent No. 6607879
                                                                                                                                                                             APPLICANT: COCKS, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J Seilhamer
TITLE OF INVENTION: COMPOSITION FOI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSED: INCYTE PHARMACEUTICAL,
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P
TELECOMMUNICATION INFORMATION
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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us-09-939-853a-75.p2n.rni

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                                                                                                                                                                                                                                   391 TCCCGGACTGAAACGGACTTGTCCTTCAAGAAAGGAGAACGCCTGCAGATTGTCAACAAC 450
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                                                                5 ProSerArgArgLysSerLeuProSerProSerLeuSerSerValGlnGlyGlnGly 24
                                                                                                                                  ProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeuGlySerPhePro 44
                                                                                                                                                                                                                                                                   65 ---AspGlyAspTrpThrValLeuSerGluValSerGlyArgGluTyrAsnIlePro
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                                                                                                                                                                                                   45 AlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrIleValSerGlu
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                                                                                       317 CCGTTACGTCGCCGCAGCGTGCCGGGGCACTGGCTGGCGGCGTCACC--
                                  US-09-939-853A-75 (1-261) x US-09-470-881-2 (1-1759)
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; Sequence 1, Application US/07820011A
; Sequence 1, Application US/07820011A
; Patent No. 5336615
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Oseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 ATC 1113
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                   GGGATTGGGGTGACCCTGTTCATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGAC 432
                                                                                                492
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                                                                                                                                                                                                                                                                                                513 AGGCAGCTGCTTTCACCAGGCAACCCCCAGGGGGCCTTTCTCATTCGGGAAAGCGAGAC 672
                                                                                                                                                                                                                                                                                                                                                                673 accaaaddrgccracrccrcrcrcrcccagacrgggarcagaccagaggggrcargrg 732
                                                                                                                                                                                                                                                                                                                                                                                                  146 ArgHisTyrArglleHisCysLeuAspAsnGlyTrpLeuTyrIleSerProArgLeuThr 165
                                                                                                                                                                                                                                                                                                                                                                                                                          PheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAlaAspAspIleCysCys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-470-881-2

Sequence 2, Application US/09470881

Sequence 2, Application US/09470881

Sequence 2, Application US/09470881

Sequence 3, Application US/09470881

APPLICANT: CHERESH, David A.

APPLICANT: ELICEIRI, Brian

TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF TITLE OF INVENTION: YES TYROSINE XINASES

TITLE OF INVENTION: YES TROSINE XINASES

TITLE OF INVENTION: YES TROSINE XINASES

TITLE OF INVENTION: YES TROSINE XINASES

TITLE OF INVENTION: YES TROSINE XINASES

CURRENT APPLICATION NUMBER: US/09/470,881

CURRENT PAPLICATION NUMBER: PCT/US99/11780

PRIOR PILING DATE: 1999-05-29

PRIOR PILING DATE: 1999-05-29

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 2

LENGTH: 1759

MANDEL OF SEQ ID NO 2

LENGTH: 1759
20
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                                                                                                                                89
                                                                                                                                                                                             90 Val------SerHisGlyTrpLeuTyrGluGlyLeuSerArgGluLysAlaGlu
70 ThrValLeuSerGluValSerGlyArgGluTyrAsnIleProSerValHisValGlyLys
                                                                                                                                                                                                                      GAGGCTCGGTCTCTCAGCTCCGGAAAAACTGGCTGCATTCCCAGCAACTACGTGGCCCCT
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                                                            LeuSerLeuArgleuGlyGluProLeuThrileValSerGlu---AspGlyAspTrpTrp
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: gene
LOCATION: (1)..(1759)
OTHER INFORMATION: chicken c-SRC cDNA
NAME/KEY: CDS
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289.00
47.33%
30.60%
21.36%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                            373
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760 GGACTCGCCAAGGACGCGTGGGAAATCCCCCGGGAGTCGCTGCCGCTGGGGAGGTGAAGGTGGTGGAAGTCGTG
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                                                                                                                                                          400 ÁGÍBACTRIGÍCGCGCCCTCAGACTCCATCCAGGCTGAAGAGÍGGTACTTTGGGAAGATC 459
                                                                                                                                                                                                                                                                                                                                                                              140 AlaSerTrpAspArglleArgHisTyrArglleHisCysLeuAspAsnGlyTrpLeuTyr 159
                                                                                                                                                                                                                                                                                                                                                                                                                         580 GCCAAGGGGCTCAATGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCGCTTCTAC 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ileSerProArgLeuThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 GCTGATGGCTTGTGCCACCGCCTGACCAACGTCTGCCCCACGTCCAAGCCCCAGACCCAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 ---ValLeuGlnArgAlaGlyProLeuProGlyLysAspIleProLeuProValThrVal 210
                                                                                                                                                                                                      100 SerArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeu
                                                                                                                                                                                                                                65 --- AspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyrAsnIlePro
                                                                                                                84 SerValHisValGlyLys------ValSerHisGlyTrpLeuTyrGluGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALX-101PCT
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SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTUS93-00445-1
Sequence 1, Application PC/TUS9300445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUBBR: 07/820,011
FILLING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) PRE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760
COMPUTER: DELL 486/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Klee, Maurice M.
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connecticut
USA
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COUNTRY: US
ZIP: 06430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCGGACTGAAACGGACTTGTCCTTCAAGAAGGAGAACGCCTGCAGATTGTCAACAAC 339
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    Genetically Engineered Endothelial Cells Exhibiting Enhanced Migration and Plasminogen Activator Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 CCGTTACGTCGCCGCAGCGTGCCGGGGCACTGGCTGGCGGCGTCACC--
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
COMPUTER: IBM PC XT
COPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Takeya, Tatsuc
AUTHORS: Handerda, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to th
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
                                                                                                                                                                                                                                                                                                                                                                                                               FILLING DATE: 1992016
CLASGIFICATION: 43.5
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: 18101
TELECOMMUNICATION INFORMATION:
TELEFRAN: (203) 255 1400
TELEFRAX: (203) 255 1400
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Genetically TITLE OF INVENTION: Bndothelia TITLE OF INVENTION: Migration TITLE OF INVENTION: and Plasmin NUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: Maurice M. Klee STRET: 1991 Burr Street CITY: Fairifield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1602 base pairs
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51.28%
34.62%
21.21%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                         06430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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Molecular and Cellular Biology
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Patent No. 5336615
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STREET: 1951 Bur Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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TYPE: NUCLEIC ACID
STRANDEDNESS: Double
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JOURNAL: Molecular
VOLUME: 5
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POSITION IN GENOME:
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US-07-820-011A-3
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ONGANISM: Gallus, gallus

PUBLICATION INFORMATION:

AUTHORS: Takeya, Tatesu

AUTHORS: Hanafusa, Hidesaburo

TITLE: Structure and Sequence of the

TITLE: Cellular Gene Homologous to the RSV src

TITLE: Gene and the Mechanism for Generating the

TITLE: Transforming Virus

VOLUME: 32
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                             LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECTLE TYPE: CDNA to MENA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ. ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287.00
51.28%
34.62%
21.21%
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Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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192 ----ValLeuGlnArgAlaGlyProLeuProGlyLysAspIleProLeuProValThrVal 210
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700 GCTGATGGCTTGTGCCACCGCCTGACCAACGTCTGCCCCACGTCCAAGCCCCAGACCCAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MaCri, Joseph A.
APPLICANT: MaCri, Joseph A.
APPLICANT: Macri, Joseph A.
APPLICANT: Macri, Joseph A.
APPLICANT: Withringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endochelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
UMBER OFS ENQUENCES: 4
NOMBER OFS EQUENCES: 4
ADDRESSEE: Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                               211 GlnArgThrProLeuAsnTrpLysGluLeuAspSerSerLeu 224
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PUBLICATION INFORMATION:
AUTHORS: Andersom, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Haing-Jian
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Acid Sequence and Derived Amino
TITLE: the Carboxy-Terminal Two-Thirds of
TITLE: the Carboxy-Terminal Two-Thirds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/ABRATION: WARE: 30,399
REFERENCE/DOCKET NUMBER: 10-101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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AsnGlyTrpLeuTyrileSerProArgLeuThrPheProSerLeuGlnAlaLeuValAsp 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 AGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTG 573
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154 TATTITGGCAAGATCACAGACGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArglysSerLeuProSerProSerLeuSerSerSerValGlnGlyGlnGlyProValThr
                                                                                                                                           DNA Sequence Encoding the
Amino-Terminal Region of the Human c-src
Protein: Implications of Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                  Divergence among src-Type Kinase
                                                                                                                                                                                                                                     Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                  AUTHORS: Arthur, Richard R. AUTHORS: Anderson, Stephen AUTHORS: Kung, Hsing-Jien AUTHORS: Fujita, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                    276.50
46.15%
30.42%
20.44%
DATE: May, 1985
PUBLICATION INFORMATION
                                                                                                                                         TITLE: DNA SequenTITLE: Amino-Term
TITLE: Protein: ITTILE: Divergence
TITLE: Oncogenes
JOURNAL: Molecula
                                                                                                                                                                                                                                                                        ISSUE: 5
PAGES: 1978-1983
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                 AUTHORS:
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US-07-820-011A-3
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Search completed: February 20, 2004, 11:33:00 Job time : 120 secs

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APPLICANT: Liao, X. Charlene
APPLICANT: Sheng, Ning
TITLE OF INVENTION: Cloning of a No. US20030059924A1el Inhibitor of Antigen-receptor
TITLE OF INVENTION: Retroviral-based Functional Screen
FILE REFERENCE: A-70219-1/RMS/DHR
Sequence 953, App
Sequence 13102, A
Sequence 13102, App
Sequence 191, App
Sequence 951, App
Sequence 951, App
Sequence 1983, App
Sequence 1983, App
Sequence 1011, App
Sequence 1711, App
Sequence 1716, App
Sequence 1776, App
Sequence 114, App
Sequence 1176, App
Sequence 31, Appl
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Sequence 184, Appl
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CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/260,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10043649 Publication No. US20030059924A1 GENERAL INFORMATION:
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APPLICANT: Mendenhall, Marcy K.
APPLICANT: Pardo, Jorge
APPLICANT: Spencer, Collin
APPLICANT: Fu, C. Alan
APPLICANT: Luo, Ying
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Mancebo, Helena S.Y.
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Shen, Mary
Liao, X. Charlene
Sheng, Ning
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-Q=/CGIDZ 1/USPTO spool p/US0993983/runat_19022004_145341_24590/app_query.fasta_1.455
-DS=Published Applications.NA -OFMT=fastap -SUFFIX=pin.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -FND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcto -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09938853 @CGN i 1 333 @runat 19022004 145341_24590
-NCPUe-C -ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WART -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=12 -WARN TIMEOUT=3 -THRANS=12 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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| cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seg:*
| cgn2 6/ptodata/2/pubpna/BCS NEW PUB.seg:*
| cgn2 6/ptodata/2/pubpna/BCS NEW PUB.seg:*
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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LENGTH: 786
                                                                       TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                               NAME/KEY: CDS
LOCATION: (1)...(786)
CTHER INFORMATION:
US-10-043-649-1
                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 933, Application US/09867550

| Sequence 933, Application US/09867550
| Patent No. US20020082206A1
| GENERAL INFORMATION:
| APPLICANT Leach, Martin D. APPLICANT Leach, Martin D. APPLICANT Leach, Martin D. Septicant Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT Law, Debie | APPLICANT SOURCE: 21402-013 (Cura-113) | TITLE OF INVENTION: Thereby | TITLE OF INVENTION: Thereby | TITLE OF INVENTION NUMBER: US/09/867,550 | CURRENT FILING DATE: 2001-09-20 | CURRENT FILING DATE: 2001-05-30 | NUMBER OF SEQ ID NOS: 2125 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 953 | Lawrent APPLICATION NUMBER: Mindows Version 4.0 | SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO 953 | Lawrent APPLICATION NUMBER OF SEQ ID NO
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GENERAL ANTOCRATION:
APPLICANT: Mehraban, Fuad,
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: Law, Debbie
APPLICANT: No. US20020082206Alel Polynucleotides from Atherogenic Cells and ITITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: UNMERR: US/09/867,550
CURRENT FILING DATE: 2001-09-20
UNMER: PRING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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; NAME/KBY: misc_feature
; LOCATION: (1)
; COCATION: (1)
; OTHER INFORMATION: Wherein n is one of a or t or c or US-09-867-550-1915
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810 CGGGAGAGCCAGAAGAGAGTCC 836
                                                                                                                                                                     Sequence 1915, Application US/09867550 Patent No. US20020082206A1
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APPLICANT: Hopkins, Christopher M. APPLICANT: Peterson, bavid P.
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                                                                                                                                         US-09-867-550-1915
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              NESCULO, Application US/09814353
Sequence 21302, Application US/09814353
FUBLICATOR NO. US2003165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Liblie, James
APPLICANT: Liblie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION: THERAPY OF COVARIAN CANCER, TITLE OF INVENTION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
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Conservative:
Mismatches:
Indels:
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) LOCATION: 1, 2, 3, 32, 862, 863, 8

; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-21302
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ORGANISM: Homo sapiens
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Best Local Similarity:
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ORGANISM: Homo
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| CCCCTGCCCAACCCGGAGGACTGGAATAGCGACTTCCTTGCCGTGCTAAGTGACTACCCG 1217
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           APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: GENER REGULATED IN ACTIVATED T CELLS
FILE REFERENCE: PA-0042 US
CURRENT APPLICATION NUMBER: US/10/002,600
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/243,521
PRIOR APPLICATION NUMBER: 60/243,521
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PERL PROGRAM
SEQ ID NO 91
LENGTH: 3756
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101
46
94
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                              Indels:
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; OTHER INFORMATION: Template ID: 059263.15
(S-10-002-600-91
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488.00
57.20%
39.30%
Cocks, Benjamin G.
                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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                                                                                                                                                                                     TYPE: DNA
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer

TITLE OF INVENTION: Sets

FILE REFERENCE: 889290-76

CURRENT APPLICATION NUMBER: US/60/233,617

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

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84 CCCCTGCCCAACCCGGAGGGACTGGATAGCGACTTCCTTGCCGTGCTAAGTGACTACCCG 143
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24 CCAGGGAAAAAAAAAAAAAAAAAAAACAGCATGCGCTGCGAGAGG 83
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                                                                                                                                                                                                             1791 AGCTATGGCCTTCGAGAGAGCATTGCCTCTTACCTGTCCCTGACCAGTGAG 1841
                                                                                                                                                            SerGluGlyLeuArgGluSerLeuSerPheTyrIleSerLeuAsnAspGlu 254
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Matches:
Conservative:
Mismatches:
Indels:
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225 LeuPheSerGluAlaAlaThrGly.
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Best Local Similarity:
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APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
APPLICANT: Rajan, Prithi
PITILE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
PILE REFERENCE: 3235/1J795-US3
                                                                                  276
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157 ATGGGAAGTCTGCCCAGCAGAAGAAATCTCTGCCAAGCCCAAGCTTGAGTTCCTCTGTC 216
                                                                                                                                                                                                                                                                                                                                                                               101 ArgGluLysAlaGluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIle 120
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                                                                                                                                                         61 IleValSerGluAspGlyAspTrpTrpThrValLeuSerGluValSerGlyArgGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                            370 AGGGAGAAAGCAGAAGAAACTGCTGTTACCTGGGAACCCTGGAGGGCCTTCCTCATC
                                                                                  217 caaggccagggaccrgrgaccarggaagcagagaagaagcaaggccacagccgrggccrg
                                                                                                                            41 GlySerPheProAlaGlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThr
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                                            GlnGlyGlnGlyProValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeu
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Matches:
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/315,150
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR PILING DATE: 2001-01-18
PRIOR PILING DATE: 2001-11-14
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/10175523 Publication No. US20030096264A1 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
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APPLICANT: Evans, David
APPLICANT: Hook, Derek
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ORGANISM: Homo sapiens
US-10-175-523-50
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Typer, James
APPLICANT: Typer, James
APPLICANT: Typer, James
APPLICANT: Typer, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REPERBING: 21402-013 (Cura-313)
FILE REPERBING: 21001-09-20
CURRENT APPLICATION NUMBER: US09/867,550
CURRENT APPLICATION NUMBER: USN 60/208,427
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 951
LENGTH: 444
                                                                                                                                                                                                                                                                                    264 ATATGIGIGGCAGAGTTTACCATGGCTGGCTGTTTGAGGGCCTGGGCAGAGACAAGGCC 323
                                                                                                               ThrargargGlySerTyrSerLeuSerValargLeuSerArgProAlaSerTrpAspArg 144
                                                                                                                                                                                                                                                       IleArgHisTyrArgIleHisCysLeuAspAsnGlyTrpLeuTyrIleSerProArgLeu 164
                                                                                                                                                                                                                                                                                                                                       ThrPheProSerLeuGlnAlaLeuValAspHisTyrSerGluLeuAlaAspAspIleCys 184
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                                                                                      GluGluLeuLeuLeuLeuProGlyAsnProGlyGlyAlaPheLeuIleArgGluSerGln 124
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76.80%
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; ORGANISM: Homo sapiens
US-09-867-550-951
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Best Local Similarity:
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Pred. No.:
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US-09-939-853A-75 (1-261) x US-10-159-563-343 (1-2298)
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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COTHER INFORMATION:
US-10-193-720-1
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ORGANISM: Homo
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GENERAL INFOARTAINS

GENERAL AND ABELICANT: Ringner, Markus

APPLICANT: Reference, Carsten

APPLICANT: Meterer, Paul

TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR

TITLE OF INVENTION: DIAGNOSTS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

TITLE OF INVENTION: 10.16.13.50/10.116.3.50/3

CURRENT FILING DATE: 2002-12-09

PRIOR PRILOK DATE: 2002-04-25

NUMBER OF SEQ ID NOS: 444

SOUTWARE: Patentin version 3.1

SEQ ID NO 343

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546 TATGIGGCCAAACTCAACACCTTAGAAACAGAAGAGGGTTTTTCAAGGATATAACCAGG 705
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                                                                                                                                           326 ATCCACCCGGACGACTIGICITTCAGAAAGAAGAAGAAGAAGAAGAAGAGGAGGAGGAG
                                                                                166 CAAACTAAAGATCCAGAGGAACAAGGAGACATTGTGGTAGCCTTTGTACCCCTATGATGGC
                                                                                                                 46 GlyGlyProAlaGluLeuSerLeuArgLeuGlyGluProLeuThrlleValSerGluAsp
                                                                                                                                                                                 GlyAspTrpThrValLeuSerGluValSerGlyArgGluTyrAsnIleProSerVal
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                                                  ValThrMetGluAlaGluArgSerLysAlaThrAlaValAlaLeuGlySerPheProAla
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o. US20040009154A1
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CORGANISM: Homo sapiens
US-10-159-563-343
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Query Match:
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Publication No. US20
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Friera, Annabelle M.
APPLICANT: Friera, Annabelle M.
APPLICANT: Mong, Exian R.
APPLICANT: Masuda, Estaban
APPLICANT: Masuda, Estaban
APPLICANT: Powell, Mark
TITLE OF INVENITON: Modulators of Leukocyte Activation, HCk Compositions and Methods
FILE REFERENCE: A-71313/RMS/DHR
CURRENT APPLICATION NUMBER: US/10/193,720
CURRENT FILING DATE: 2002-11-27
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SerArgArgLysSerLeuProSerProSerLeuSerSerValGlnGlyGlnGlyPro
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337 TCTGAGGACATCATCGTGGTTGCCCTGTATGATTACGAGGCCATTCACCACGAGGACTC 396
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
LENGTH: 2015
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APPLICANT: Alexander H. Borchers; APPLICANT: Kenneth W. Dobie
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360.50
58.38%
41.62%
26.64%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                               US-09-954-456-1983
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| Sequence 1983, Application US/09954456
| Patent No. US20020115057A1
| GENERAL INFORMATION:
| APPLICAMT: Young, Paul
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: WHERE: US/09/954,456
| CURRENT APPLICATION NUMBER: US/60/233,617
| PRIOR APPLICATION NUMBER: US/60/234,052
| PRIOR APPLICATION NUMBER: US/60/234,052
| PRIOR FILING DATE: 2000-09-18
| PRIOR FILING DATE: 2000-09-18
| PRIOR FILING DATE: 2000-09-18
| PRIOR FILING DATE: 2000-09-25
| PRIOR FILING DATE: 2000-09-25
| PRIOR FILING DATE: 2000-09-25
| PRIOR FILING DATE: 2000-09-25
| PRIOR PRILOR APPLICATION NUMBER: US/60/235,637
| PRIOR PRILOR DATE: 2000-09-26
| PRIOR PRILOR DATE: 2000-09-26
| PRIOR PRILOR DATE: 2000-09-26
| PRIOR PRILOR DATE: 2000-09-26
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                       Length:
Matches:
Conservative:
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION FILE REFERENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 87
LENGTH: 2015
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Sequence 140, Application US/10252157
Sequence 140, Application No. 1203030190640A1
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Parison, Geoelia I.
IITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER FILE REFERENCE: PA-0027-1 US
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Matches:
Conservative:
Mismatches:
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| NAME/KEY: CDS
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| US-10-007-010-3
                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
TILLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS; FILE REFERENCE: PA-0026-1 CIP
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; NAME/KEX: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 411296.2
US-10-252-157-140
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CURRENT APPLICATION NUMBER: US/10/252,157
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                      CURRENT FILING DATE: 2002-10-0
PRIOR APPLICATION NUMBER: 60/29;
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL Program
LENGTH: 2341
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US-10-062-674-2038
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                      APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
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PRIOR PELLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-15
PRIOR PELLOATION NUMBER: US 60/290,645
PRIOR PELLOATION NUMBER: US 60/290,645
PRIOR PELLOATION NUMBER: US 60/290,336
PRIOR PILING DATE: 2001-05-22
PRIOR PELLOATION NUMBER: US 60/297,457
PRIOR PELLOATION NUMBER: US 60/297,457
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
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ORGANISM: Rattus norvegicus
FEATURE:
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// OTHER INFORMATION: Incyte ID No. US20040005559A1 411296.5
US-10-062-674-2038
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: US 09/625,102
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTHARE: PERL PROGRAM
SEQ ID NO 2038
LENGTH: 2343
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
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                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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304 CCGAACAGCATCAACAGCCTGCCCCGGGGTTCGTGGAGGGCTCTGAGGACACACATTGTG 363
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OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM 013185
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114 ProGlyGlyAlaPheLeulleArgGluSerGlnThrArgArgGlySerTyrSerLeuSer 133
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Search completed: February 20, 2004, 12:38:07 Job time : 370 secs

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February 19, 2004, 21:21:18; Search time 87.562 Seconds (without alignments) 9899.970 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES ID	AX443199 AX443133																																20 bp DNA stent WO0216599.				P.B., Grosse, W.M., I k, K.A., Szekeres, E.S	аше
* Query Match Length DB	20	00.0 1183	00.00 2567	00.0 2788	00.0 145833	7.0 80828	7.0 108742	7.0 110000	7.0 129218	7.0 133181	7.0 140410 7.0 145493	7.0 146061	7.0 1451/5	7.0 149397	7.0 152445 7.0 152782	7.0 154803	7.0 155537 7.0 156527	7.0 158755	7.0 159184 7.0 160994	7.0 161000	7.0 161279 7.0 161460	7.0 161460	7.0 161671	7.0 161957	7.0 162703	7.0 165211 7.0 165211	7.0 167663	7.0 168547	7.0 169082 7.0 169082	00	1		3199 ence 140 from Patent	ָט	necic construct hetic construct ficial communication	educinos ini	, C.E., 8, R.A.,	J.N. an Is and n
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Patent: Curagen

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FEATURES

1..20 /organism="synthetic construct" /wol_type="unassigned DNA" /db_xref="taxon:32630" /noTe="oligonucleotide primer"

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Query Match Best Local

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Matches

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DNA

AX443133 1183 bp Sequence 74 from Patent WO0216599.

AX443133.1 GI:21690555

RESULT 2
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DEFINITION
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VERSION
KEYWORDS
SOURCE

Homo sapiens (human) Homo sapiens

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Dy: Sequencing Group at the Stanford Human Genome
DNA Sequencing Dy: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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Series: IRAK Plate: 88 Row: a Column: 20
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (23-DEC-2002) National Institutes of Health, Mammalian
Submitted (23-DEC-2002) National Institutes of Health, Mammalian
Cana Callection (MGC), Cancer Genomics Office, National Cancer
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proteins and mucleic acids encoding same Patent: WO 0216599-A 76 28-FEB-2002;

Curagen Corporation (US); COR THERAPEUTICS, INC. (US)

1. 01103/Qualifiers

1. 01201/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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DNA

Sequence 76 from Patent W00216599.

AX443135.1 GI:21690556

Homo sapiens (human)

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 3 AX443135

Homo sapiens

TITLE JOURNAL

FEATURES

creacaearraeecrire 282

301

1 CTGGACAGGTTAGGGCTTTG 20

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100.0%; Score 20; DB (100.0%; Pred. No. 4.5; iive 0; Mismatches

Query Match Best Local Similarity 100.' Matches 20; Conservative

ORIGIN

/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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Gaps

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PAT 14-JUL-2003

linear

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Human DNA sequence from clone RP3-460J8 on chromosome C2041.21-11.23 Contains the 3' end of the gene for a novel protein similar to N-myc downstream regulated (NDRG1) the 5' end of a gene encoding a novel protein tyrosine kinase, ESTs, STSs and GSSs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk clone on Aug 7, 2000 this sequence version replaced gi:6425549.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 66741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S. Dugas, M., Ells, R., Brors, B. and Mergenthaler, S.
Novel genetic markers for leukemias
Patent: WO 03039443-A 3014 15-WAY-2003;
Boutsches Krebsforschungszentrum (DB);
Dudysches Krebsforschungszentrum (DB);
Dudysches Maximilian-Universitaet Muenchen (DB);
PD Dr. Dr. (DB); Schoch, Claudia (DB); Kern, Wolfgang (DB)
                                                          Score 20, DB 6, Length 2567;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 2788;
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                                                                                                                                                                                                                                                                                                  Sequence 3014 from Patent W003029443. AX780857
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100.0%; Pred. No. 4.4
Live 0; Mismatches
                                                            100.0%; Score 20; DB
ilarity 100.0%; Pred. No. 4.4
Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                                                                                                                                                 318 CTGGACAGGTTAGGGCTTTG 299
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                                                                                                                                                        1 CTGGACAGGTTAGGGCTTTG 20
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HTG; NDRGI; SH2 domain.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.0
Matches 20, Conservative
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                                                                                    Best Local Similarity
Matches 20; Conserv
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                                                                 Query Match
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VERSION
KEYWORDS
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AUTHORS
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TITLE
JOURNAL
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JOURNAL
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HS460J8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="LocusID:84174"
/translation="MGSLPSRRXSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFP
AGGPAELSLELGEPLTIVSEDGDWHYULSEVGGEYNIPSYNTYAKVSHGWIYEGLSRE
KAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRIHCLDNGWLYI
SPRLYFPSLQALVDFYSELADDICCLLKEPCYLQRAGPLPGKOIPLPVTVQRTPLNWK
ELDSSLLFSEAATGEESLLSEGLRESLSFYISLNDEAVSLDDA"
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28416422. Location/Qualifiers
1. .2538
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// note="SH3; Region: SH3 domain. SH3 (Src homology 3)
domains are often indicative of a protein involved in
signal transduction related to cytoskeletal organization.
Pirst described in the Src cytoplasmic tyrosine kinase,
/db xref="CDD:pfam00018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang, H., Yang, W.P., Wu, Y., Whitney, G.S., Perez-Villar, J.J. and Kanner, S.B.
Cloning and expression of human slap-2: a novel sh2/sh3
domain-conteaining human slap homologue having immune cell-specific expression
Patent: WO 0242457-A 1 30-MAY-2002;
Bristol-Myers Squibb Co. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                    gene="SLA2"
'note="synonyms: FLU21992, SLAP-2, C20orf156, MGC49845,
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/tlssue type="Prostate, adenocarcinoma."
/lone_lib="NIH MGC_91"
/lab host="DH108"
/note="Wector: pGWV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SH2; Region: SH2 domain"
/db_xref="CDD:pfam00017"
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                                                                                                                                                                                                                                                                                                                                          /db_xref="LocusID:84174"
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363_.1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 from Patent W00242457.
AX452880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                            . .2538
                                                                                                                                                                                                                                                                                                                                SLAP2"
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KEYWORDS
SOURCE
ORGANISM
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AX452880/c
LOCUS
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AUTHORS
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                                              PEATURES
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Gaps

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Torsten,

Schnittger, S.,

PRI 23-JUL-2001

linear

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repeat_region
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misc_feature
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polyA_site
gene
corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20

IMPORTANT: This sequence is not the entire insert of clone RP3-460J8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP3-469A13 is at 100 in this sequence. The true right end of clone RP3-460J8 is at 66741 in this sequence. The true left end of clone RP3-469A13 is at 100 in this sequence. The true left end of clone RP3-460J8 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality as as compressions and repeats; all regions were covered by high quality data (i.e., phred quality as segembly was confirmed by restriction digest. RP3-460J8 is from the firther definited by restriction digest. RP3-460J8 is from the firther definited by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="SWISS-PROT:Q9H6Q3"
'translation="MGSLPSRRKSLPSPSLSSSVQGQGPVTWEAERSKATAVALGSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(50. 544)
/note="match: GSS: Em:B45150"
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/note="match: cDNAs: Em:AK025645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Continues in Em:AL050318 as dJ977B1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="14 copies 2 mer ta 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
complement(joIn(<240. .339,6995. .7085))
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/note="15_copies 2 mer ag 93% conserved"
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/note="match: GSS: Em:AQSS6467"
complement (6985, .7492)
/note="match: GSS: Em:AQSS6478"
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'note="match: GSS: Em:AQ807191"
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/note="match: STS: Em:HS427J1S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="20"
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clone="RP3-460J8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="RPCI-3"
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complement (17523. .54534)
/gene="dJ469A13.3"
complement (join (<17523. .19451,20551. .20589,22110. .22161,
22247. .22282,26087. .26134,30796. .30847,30986. .31051,
32039. .32142,37091. .37147,46566. .46652,48268. .48328,
50163. .50225,3342. .53362,54429. .>54534)
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Em:AP159092 Em:AP14702 Em:MS9814
match: ESTS: Em:AA147402 Em:AA039000 Em:AM003952 Em:W89263
Em:AA325826 Em:AA130982 Em:AA362360 Em:AA445016
Em:AA02595 Em:T85147 Em:AA162360 Em:AA445016
Em:T780573 Em:AT186673 Em:AA13437 Em:A1004026
Em:T88705 Em:AT186673 Em:AA113437 Em:AA104711
Em:AU035165 Em:AV002368"
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/db_xref="SHISS-PROT:090GV2"
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/rennalat_non="SHOINDAPOGOGAPS-PPTGYQYPROBLABMLPPVLTHLSLKSII
GIGVQAQAYILSSRFALNHPBLVBGLVLINVDDCAKGHIDWAASKLSGLTTNVVDIILA
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KTLKCSTLLVVGDNSPAVZAVVECNSRLNPINTTLLKMADCGGLPQVVQPGKLTFAPK
YFLQGMGYIPYVQLSHLSTESVPSASMTRLARSRTHSTSSSLGSGESPFSRSVTSNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="novel protein (FLJ13556) similar to N-myc downstream regulated (NDRG1) match: proteins: Sw:Q62433 Sw:Q92597 Tr:Q9Z2L9 Sw:P97862"
                                                                                  14248. 14297
/note="MER21B repeat: matches 374. .422 of consensus"
14594. .14614
                               .3593. .13961
'note="MER21B repeat: matches 422. .785 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: cDNAs: Em:AB033922 Em:U52073 Em:D87953
                                                                                                                                                                    note="MERGIB repeat: matches 355. .374 of consensus 4746. .15078 "note="MER21B repeat: matches 1. .355 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evidence=not_experimental
product="dJ460J8.1 (continued from dJ469Al3.3 in
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|4313. .34420
|note="HY1 repeat: matches 1, .109 of consensus"
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/note="28 copies 2 mer ta 78% conserved"
34564. .34611
                                                                                                                                                                                                                                                                                                   7519. .17686
note="match: GSS: Em:AZ067993"
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complement(27980. .28556)
tt 92%
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complement(17542, .17547)
/gene="dJ469A13.3"
17555, .17811
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/qene="dJ469A13.3"
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copies 2 mer
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complement (17522)
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2. Chases to 145833)

2. Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Erown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Perreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Horband, J.C., Iliev, I., Johnson, R., Landers T., Lehoczky, J., Lehoczky, J., Lieu, C., Lilu, G., Lock, K., Mardonald, P., Marquis, N., McCharl, P., McGurch, P., McGurch, P., McGurch, P., McGurch, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., McMens, P., McGurk, A., McKernan, K., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Ollvar, T.M., Ollvar, T.M., Ollvar, T.M., Ollvar, T.M., Ollvar, T.M., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59738. .60495
/note="TIGGER2 repeat: matches 1780. .2541 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="TIGGER2 repeat: matches 2541. .2714 of consensus"
                                      .2553. .43658
note="MER52C repeat: matches 1. .1278 of consensus"
7989. .48470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note="MEK11C repeat: matches 1. .1071 of consensus"
62847. .63174
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note="24 copies 2 mer ta 79% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58856. .59001
/note="73 copies 2 mer at 83% conserved"
complement(58930. .59281)
                                                                                                                                                                                                        /note="45 copies 2 mer ta 76% conserved"
52922. .53120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: STS: Em:G07504"
complement (57696. .58013)
/note="match: STS: Em:G07632 Em:G07634"
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57509. .57838
                                                                                                                                      /note="match: GSS: Em:AQ672417"
19391. .49480
                                                                                                                                                                                                                                                                         /noce="match: STS: Em:G04621"

Complement (53426. .54032)

/gene="d4469A13.3"

/noce="match: GSS: Em:AQ314824

match: STS: Em:GSS5853"
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Homo sapiens (human)
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Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, M., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tricall, A., Travers, M., Trigillo, J., Tossillev, H., Viel, R., Vola, R., Wilson, B., Wu, K., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Direct Submitssion

Besearch, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 27, 2000 this sequence version replaced gi:7283243.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.gencme.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                       ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                        Center project name: L7115 Center project name: L7115 N 14

Center clone name: T72 N 14

Sequencing vector: M3; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 125577 bases at least Q40

Consensus quality: 135703 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 14233; sum-of-contigs

Quality coverage: 2.6 in Q20 bases; sum-of-contigs

Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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Web site: http://www-seq.wi.mit.edu
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db_xref="taxon:9606"
chromosome="20"
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Frinishing Completed at Stanford Human Genome Center
www.shgo.stanford.edu

Waw.shgo.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Brrors is 0.4.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 147.2kb). It is clipped at the overlap with AC010237.
The number of bases overlapped is 38259.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 8028)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (26-FBE-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94599, USA
On Feb 26, 2002 this sequence version replaced gi:15290461.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 80828)
DOB Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Homo sapiens chromosome 5 clone RP11-138M1, complete sequence.
ACO93247
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100.0%; Score 20; DB 2; Length 145833;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
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DOE Joint Genome Institute.
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Gaps

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Length 100300; Indels

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us-09-939-853a-140.rge

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Pred. No. 1.2e+02;
0; Mismatches 1;
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Center clone name: CITB-E1_2565N12
                          /organism="Homo sapiens"
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Center Code: JGI
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100300 bp DNA linear HTG 14-MAR-2002
Homo sapiens chromosome 5 clone RP11-388B4, WORKING DRAFT SEQUENCE,
And the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the con
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Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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Consensus quality: 97011 bases at least Q30
Consensus quality: 97011 bases at least Q30
Consensus quality: 9705 bases at least Q20
Estimated insert size: 99700; sum-of-contigs estimation
Quality coverage: 9.62 in Q20 bases; agarose-fp estimation
Quality coverage: 16.88 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 7 contigs: The true order of the places
* is not known and their order in this sequence record is
                                                                                                                                                                                       Gabs
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                                                                                                                 Score 17.4; DB 9; Length 80828;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0;
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4: contig of 1499 bp in length
4: aga of unknown length
6: contig of 4404 bp in length
8: gap of unknown length
1: contig of 11003 bp in length
1: gap of unknown length
1: gap of unknown length
3: contig of 13618 bp in length
3: gap of unknown length
3: gap of unknown length
3: gap of unknown length
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of 62605 bp in length
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contig of 4976 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC114970.1 GI:19424431
HTG; HTGS_PHASB1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOMO sapiens (human)
HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.jgi.doe.gov
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/chromosome="5"
/clone="RP11-138M1"
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JOB Joint Genome Institute.
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0
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                                                                                                                    87.0%;
ilarity 94.7%;
Conservative 0
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3194:
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32620
37596
37696
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Best Local Simil
Matches 18; (
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
AC114970
LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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COMMENT

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Consensus quality: 107872 bases at least Q40
Consensus quality: 108423 bases at least Q30
Consensus quality: 108423 bases at least Q30
Consensus quality: 108423 bases at least Q30
Estimated insert size: 137000; agarose-fp estimation
Estimated insert size: 137000; agarose-fp estimation
Quality coverage: 8.13 in Q20 bases; sque-of-contigs estimation
Quality coverage: 10.27 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the places
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor:
* provided by the submittor:
* This sequence will be resplaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 131414 31513: gap of unknown length
ACC23817 108742 bp DNA linear HTG 07-MAR-2002 Homo sapiens chromosome 5 clone CTD-2565N12, WORKING DRAFT SEQUENCE, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 108742)

DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 7, 2002 this sequence version replaced gi:18139273.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butherla, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 108742)
DOE Joint Genome Institute.
                                                                                                                                                                                           ACO23817.5 GI:19224766
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Consensus quality: 124109 bases at least Q40
Consensus quality: 125106 bases at least Q30
Consensus quality: 12593 bases at least Q30
Consensus quality: 12593 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 178018; sum-of-contigs estimation
Quality coverage: 8 in Q20 bases; agarose-fp estimation
Quality coverage: 12.03 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* trus of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Homo sapiens chromosome 5 clone RP11-1310P17, WORKING DRAFT
SACHSOCE, 13 unordered pieces.
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Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 15918)
10 Joint Genome Institute.
Sequencing of Human Chromosome 5
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                                                                                                                                                                                                                                                                                               Length 116702;
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AC138851.1 GI:27805263
HTG; HTGS PHASE1; HTGS_ACTIVEFIN.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                           Score 17.4; DB 9;
Pred. No. 1.2e+02;
0; Mismatches 1;
      Estimated Total Number of Errors is 0.
                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/mb_xref=rtaxon:9606"
/chromosome="5"
/clone="CTC-202015"
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Center clone name: RPCI-11_1310P17
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Center: Joint Genome Institute
Center Code: JGI
                         location/Qualifiers
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DOE Joint Genome Institute.
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Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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7830
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KEYWORDS
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AC138851/c
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        Sequence split into 4 fragments
        LOCUS AC139485 Accession AC139485

        Pragment Name
        Begin
        Ind

        AC139485 0
        1 10000

        AC139485 1
        100001
        210000

        AC139485 2
        200001
        310000

        AC139485 3
        300001
        368755

        Continuation (2 of 4) of AC139485 from base 100001 (AC139485 Homo sapiens chromosome 5

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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTC-202015, complete sequence
AC132801
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                             Score 17.4; DB 2; Length 108742;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0:
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hinishing Completed at Stanford Human Genome Center
www.shgo.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
14 101416: contig of 69903 bp in length 7 101516: gap of unknown length 7 108742: contig of 7226 bp in length.
                                                                                                                                                                                                                                                                     /clone="CTD-2565N12"
/clone_lib="CalTech human BAC library D"
                                                                                                                           1. .108742
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="texon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                       87.0%;
ilarity 94.7%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity
      31514
101417
101517
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AC132801/c
LOCUS
DEFINITION
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AUTHORS
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AC139485 1
WPCOMMENT
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JOURNAL
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AUTHORS
                                                                                              FEATURES
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Search completed: February 19, 2004, 23:23:17 Job time : 91.562 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC138930 133181 bp DNA linear HTG 21-JAN-2003
Homo sapiens chromosome 5 clone RP11-678014, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 133181)
Direct Submission
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133181)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 131745 bases at least Q40
Consensus quality: 131928 bases at least Q30
Consensus quality: 132052 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 13781, sum-of-contigs estimation
Quality coverage: 13.96 in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.0%; Score 17.4; DB 2; Length 129218; Best Local Similarity 94.7%; Pred. No. 1.2e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0;
                                                                  contig of 10702 bp in length
gap of unknown length
contig of 4185 bp in length
gap of unknown length
contig of 19818 bp in length
gap of unknown length
                                                                                                                                                                                                           gap of unknown length contig of 28480 bp in length gap of unknown length contig of 9245 bp in length gap of unknown length
                                                                                                                                gap of unknown length
contig of 19818 bp in length
gap of unknown length
contig of 5192 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                      0 129218: contig of 26599 bp in length.
                  known length
3330 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="5"
/clone="RP11-1310P17"
/clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_ACTIVEFIN HTGS_ACTIVEFIN HTGs ACTIVEFIN
                                                       length
                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 1555206
Center clone name: RPCI-11_678014
                                                                                                                                                                                                                                                                                                                                                 1. .129218
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Code: JGI
Web site: http://www.jgi.doe.gov
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contig
gap of
                                                          gap of
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102619:
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35199:
39384:
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35100
35200
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59403
64595
                                                          24298
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AC138930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRIGIN
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Quality coverage: 18.4 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 17.4; DB 2; Length 133181; llarity 94.7%; Pred. No. 1.2e+02; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                    1 1094: contig of 1094 bp in length
1095 1194: gap of unknown length
1295 2421: contig of 1227 bp in length
1522 4100: contig of 1579 bp in length
1510 4200: gap of unknown length
1511 23545: contig of 19345 bp in length
1546 23645: gap of unknown length
1546 133181: contig of 109536 bp in length
1550 15001111: contig of 109536 bp in length
1550 15001111: contig of 109536 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .133181
/ Organism="Homo sapiens"
/ Mol_type="genomic DNA"
/ db_xref="taxon:9606"
/ chromosone="R5"
/ clone="RP11-678014"
/ clone_lib="RPCI human BAC library 11"
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Matches 18; Conserv
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GenCore version 5.1.6
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February 19, 2004, 21:15:48; Search time 18.5292 Seconds	(without alignments)	4585.415 Million cell updates/sec	
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1 ctggacaggttagggctttg 20 US-09-939-853A-140 20 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04: genesegn1980s:* Database :

geneseqn2001as:* geneseqn2001bs:* geneseqn2003bs: geneseqn2003as: geneseqn1990s:* geneseqn2000s:* geneseqn2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

SUMMARIES

Description	Abk61505 Human NOV	Human	DNA en	_	Abk61465 Human cDN	Aad43980 Human Src	4 Filame	σ.		Ada53227 Human cod	O Human	m	Human	5 Human	Human	0 Human	Human	5 Human	Ach48692 Human leu	Ach40016 Human foe	Human	4 Human	Aax14434 H. pylori
di ID	ABK61505	ABQ98669		ABQ98670		AAD43980		ABZ56309	AAF14531	ADA53227	ADA02960	ADB72698	ADC85440	ADE57896	ADE57892	ADE57900	ADE57904	ADE83385	ACH48692	ACH40016	ACD95832	ABA16524	AAX14434
* Query Match Length DB	20 6	4	445 5	763 6	1183 6	2567 6	538 9	589 7	809 3	2305 7	44325 8	44325 9	44325 9	2446 9	2446 9	2446 9	2446 9	2446 9	403 8	467 8	712 7	н	1152 2
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	82.0	82.0	82.0	82.0	82.0	79.0	79.0	79.0	79.0	79.0
Score	20	20	50	20	20	20	16.8		16.8	16.8	16.8		16.8	16.4	16.4	16.4	16.4	•	٠	٠		15.8	15.8
Result No.	। ਜ	0	m	Ω 4,	n n	o U	0	ω U		υ 10	c 11	-	a 13	14	12	16	17	18	19	20	21	22	23

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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	0000	U	U	00

ALIGNMENTS

ABK61505 standard; DNA; 20 BP. Human NOV13 RT-PCR primer #1. (first entry) 18-JUN-2002 ABK61505; RESULT 1 ABK61505

Human; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; cell signal processing disorder; metabolic pathway modulation disorder; dalabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; primer; uterus cancer; immune response; graft-versus-host disease; Exon linking; acquired immunodeficiency syndrome; AlDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy; reverse transcriptase PCR.

WO200216599-A2 Homo sapiens. 28-FEB-2002

25-AUG-2000; 2000US-0228191P. 08-FBB-2001; 2001US-0267300P. 20-FEB-2001; 2001US-026961P. 20-MAR-2001; 2001US-0277337P.

27-AUG-2001; 2001WO-US026510.

Shimkets RA; Grosse WM, Hart M, Kekuda R, Shir Tomlinson JB, Topper JN, Yang R; (CURA-) CURAGEN CORP. (CORT-) COR THERAPEUTICS INC. Burgess CE, Conley PB, Spytek KA, Szekeres ES,

WPI; 2002-280937/32.

New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.

Example 2; Page 234; 263pp; English.

The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX, a NOVX variant (differing by no more than 15%), the nucleotide

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encoding NoVX (or its complement, fragment or variant). NoVX is NoV1-14, 154, 155, 163, and 16b. The NoVX polypeptide, nucleic acid encoding it and antibody against it, are useful for treating or preventing (e.g. by gene therapy) a NoVX-associated disorder in humans, e.g. cardiomyopathy, attentional conference or cancers. The NoVX polypeptide are tabolic pathway modulation, diabetes or cancers. The NoVX polypeptide are and nucleic acids are also useful for determining the presence of predisposition to the diseases. The NoVX nucleic applications for predisposition to the diseases. The NoVX nucleic applications for especially useful in therapeutic or prophylactic applications for disorders associated with aberrant NoVX expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancer), immune response, graft-versus-host disease, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, congenital heart defects, multiple sclerosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic or prognostic assays, or human disorders, as well as in diagnostic spilications. The present sequence is a reverse transcriptase (RT)-PCR primer used to measure treature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
           $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Score 20; DB 6; Length 20;
Pred. No. 1.7;
; Mismatches 0; Indels
                                                                1 CTGGACAGGTTAGGGCTTTG 20
                                                                                                  1 crócacacaciraciócirric 20
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0
Query Match

Best Local Similarity 100.0%;
Matches 20; Conservative 0
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ABQ98669 standard; DNA; 444 BP (first entry) 04-NOV-2002 ABQ98669;

Human ORF476 coding sequence.

Cytostatic, Cardiant, Anti-allergic, Immunosuppressive, Vulnerary, Antinfiammatory, gene therapy, human, ORFX, atherogenic, platelet, human umbilical vein endothelial cell; HUVEC, atherosclerotic plaque, cancer, cardiovascular disease, allery, autoimmune disease, wound healing, blood coagulation disorder; inflammatory disorder; ds.

Homo sapiens

27-JUN-2002.

US2002082206-A1.

30-MAY-2001; 2001US-00867550.

30-MAY-2000; 2000US-0208427P

(LEAC/) LEACH M D. (MEHR/) MEHRABAN F. (CONL) CONLEY P B. (TOPP/) TOPPER J N. (LAWD/) LAW D.

Topper JN, Conley PB, Leach MD, Mehraban F,

ñ Law

WPI; 2002-626554/67. P-PSDB; ABP64106.

New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including

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                                                                                          The present invention relates to novel human ORFX polypeptides and their coding sequences (ABR63611-ABP64681 and ABD69819-4-AB099567). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological condition associated with an ORFX associated discorder, e.g. cancer, cardiovascular disease, allery, autoimmune disease, wound healing, blood coagulation disorders or inflammatory disorders. Note: The sequence data obtained in electronic forms directly from the USPTO web site at sequence. Luspto.gov/sequence.html?PocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder;
cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 6; Length 444; 100.0%; Pred. No. 2.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Seguence 444 BP; 103 A; 128 C; 132 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #10551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 10551; 103pp; English.
                                                           Claim 2; SEQ ID NO 951; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 CTGGACAGGTTAGGGCTTTG 41
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABG10560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS74747;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS74747
ID AAS7
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genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) iss useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful In medical imaging of bites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Ab564197-Ab54564 represent novel human diagnostic coding sequences. Ab564197-Ab54564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from MPD at the printed appearation, but was obtained in electronic format directly from MPD at the wippoint whip of the wippoint appearation and port sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 445 BP; 89 A; 112 C; 143 G; 101 T; 0 U; 0 Other;
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Match 100.0%; Score 20; DB 5; Length 445; Local Similarity 100.0%; Pred. No. 2.3; les 20; Conservative 0; Mismatches 0; Indels CTGGACAGGTTAGGGCTTTG 187 1 CTGGACAGGTTAGGGCTTTG 20 168 Query Match Best Loc Matches à 요

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Gaps ö

> Human ORF477 coding sequence. ABQ98670 standard; DNA; 763 04-NOV-2002 (first entry) ABQ98670;

Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary; Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder; ds.

Homo sapiens

JS2002082206-A1

27-JUN-2002

30-MAY-2001; 2001US-00867550

30-MAY-2000; 2000US-0208427P

(LEAC/) LEACH M D. (MEHR/) MEHRABAN F. (CONL/) CONLEY P B. (TOPP/) TOPPER J N.

LAW D. (LAWD/) Ä Law Topper JN, Conley PB, Leach MD, Mehraban F,

WPI; 2002-626554/67. P-PSDB; ABP64107 New polypeptide designated ORFX are present in human atherogenic cells and are useful to prevent and treat ORFX-associated disorders including cancer, allergy, wound healing or autoimmune, cardiovascular or inflammatory disease.

Claim 2; SEQ ID NO 953; 78pp; English.

The present invention relates to novel human ORFX polypeptides and their

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; call signal processing disorder; metabolic pathway modulation disorder; diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; uterus cancer; immune response; graft-versus-host disease; arguired immunodeficiency syndrome; AIDS; asthma; Crohn's disease; hypertension; congenital heart defects; multiple sclerosis; inflammation; Albright hereditary osteodystrophy.
                                                                                                                                                        data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide (NOVX) a mature form of NOVX. As NOVX variant (differing by no moore than 15%), the nucleotide encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it
coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequence were discovered in human atherogenic cells, in particular in platelets and human unbilical vein endothelial cells in particular in platelets and human unbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and mucleic acids are useful for treating or preventing a pathological condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, bloo coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at sequence.html?DocID=20020082206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides for treating or preventing a disorder associated with them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.
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                                                                                                                                                                                                                                                                                                                                    Gaps
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Tomlinson JE, Topper JN, Yang R;
                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 6; Length 763; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                       Sequence 763 BP; 176 A; 222 C; 218 G; 147 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding protein NOV13.
                                                                                                                                                                                                                                                                                                                                                                                                            189 credacaderracecrire 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 98; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                            1 CTGGACAGGTTAGGGCTTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK61465 standard; cDNA; 1183 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-2000; 2000US-0228191P.
08-FEB-2001; 2001US-0267300P.
20-FEB-2001; 2001US-026961P.
20-MAR-2001; 2001US-0277337P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP. (CORT-) COR THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2001; 2001WO-US026510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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Szekeres ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-280937/32.
P-PSDB; AAU91308.
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Spytek KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JJN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK61465;
                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                    Matches
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gene therapy) a NOVA-associated disorder in humans, e.g. cardiomyopathy, at the condition disborder in humans, e.g. cardiomyopathy, and associated disorder in humans, e.g. cardiomyopathy, metabolic pathway modulation, disborder to cancers. The NOVA polypeptide and mucleic acids are also useful for determining the presence of predisposition to the diseases. The NOVA nucleic acid and polypeptide are especially useful in therapeutic or prophylactic applications for disorders associated with aberrant NOVA expression or activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus cancer), immune response, graft-versus-host disease, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension, eongenital heart defects, multiple sclerosis, inflammation or Albright hereditary osteodystrophy and many other diseases listed in the specification. The DNA encoding the protein is useful in gene therapy for treating the conditions. This is also useful in detection assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping, tissue typing, diagnostic or prognostic assays, or for developing a powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. The present sequence encodes a NOVX protein
   are useful for treating or preventing (e.g. by
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Score 20; DB 6; Length 1183; Pred. No. 2.5;); Mismatches 0; Indels C Sequence 1183 BP; 251 A; 359 C; 333 G; 240 T; 0 U; 0 Other; 100.0%; Local Similarity 100. 1es 20; Conservative Query Match

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Gaps

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0; Indels

6

Matches

crecacetracecrire 282 CTGGACAGGTTAGGGCTTTG 20 301 ઠ 셤

AAD43980 standard; cDNA; 2567 BP.

AAD43980;

(first entry) 13-DEC-2002

Human Src-Like Adapter Protein-2 (hSLAP-2) cDNA.

Human; SH2/SH3-domain-containing adapter; Src-Like Adapter Protein-2; SLSAP-2; immune disease; cancer; neoplasm; immune disorder; signal transduction; autoimmune disease; cancer; neoplasm; inflammation disorder; rheumatoid arthritis; osteoarthritis; psoriasis; rhinitis; allergy; inflammatory bowel disease; gene therapy; cofn's disease; systemic lupus erythematosus; tissue/organ rejection; multiple sclerosis; asthma; acute respiratory distress syndrome; pulmonary disorder; dermatological; neuroprotective; gene; sse.

Homo sapiens

"Human SLAP-2" Location/Qualifiers 415. .1200 /*tag= a /product=

WO200242457-A1

30-MAY-2002.

20-NOV-2001; 2001WO-US043367.

22-NOV-2000; 2000US-0252545P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Kanner SB; Perez-Villar JJ, Whitney GS, ž Chang H, Yang W,

WPI; 2002-463632/49. P-PSDB; AAE26357.

Novel substantially purified human SH2/SH3-domain-containing adapter polypeptide, termed Src-Like Adapter Protein-2, useful for therapeutic

Novel promoter DNA derived from Aspergillus genus, useful for protein

WPI; 2003-818168/77.

production

Claim 1; SEQ ID NO 145; 83pp; Japanese

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The invention relates to a substantially purified human SH2/SH3-domain-
Containing adapter polypeptide, termed Src-Like Adapter Protein-2 (SLAP-
2): The invention is useful for treating an immune disorder involving
hyperactivity of B- or T-lymphocytes in a mammal. The invention is
useful for screening for antagonists or inhibitors of the interaction of
hSLAP-2 with cellular signalling compounds, for diagnosing, treating or
preventing diseases or disorders associated with aberrant or uncontrolled
cellular signal transduction, for determining those cellular signalling
molecules which associate with hSLAP-2 and which provide critical signals
or cell activation, and as effectors in methods to affect T- cell
cor cell activation, and as effectors in methods to affect T- cell
cortivation. The invention is useful in screening assays to identity and
detect candidate bloactive agents that modulate hSLAP-2 bloactivity, for
ptential use to treat autoimmune diseases which may be caused by
conditions, diseases, or disorders, T-cell and B-cell neoplasms, conditions, diseases, or disorders, T-cell and Conditions, Theumatoid arthitis,
conditions, diseases, or disorders, T-cell and Conditions, theumatoid arthitis,
conditions, diseases, and disorders, particularly those involving
and ulcerative colitis), allergies, particularly those involving
conditions are cosinophile, acterned is pulmonary diseases including
erythematosus and multiple sclerosis, pulmonary diseases including
erythematosus and multiple sclerosis, pulmonary diseases including
erythematosus and multiple sclerosis, pulmonary diseases including
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erythematosus and multiple sclerosis, pulmonary diseases including
cuseful in gene therapy. The present sequence is human SLAP-2 cDNA
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intervention in immunological and inflammatory disorders and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filamentous fungi Aspergillus genus DNA sequence, SEQ ID No 145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter activity, filamentous fungi Aspergillus genus;
transcription activation; glucose; gene transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HGET ) HIGETA SHOYU KK.
(DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 CTGGACAGGTTAGGCTTTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGGACAGGTTAGGGCTTTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD22694 standard; DNA; 538 BP
                                               Claim 2; Fig 1; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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The invention relates to a novel DNA sequence comprising any one of 74 sequences with promoter activity, having a fully defined sequence shown in the specification or having a sequence which hybridised under stringent conditions to one of the 74 sequences. The invention further comprises one of the 74 DNA sequences or their DNA fragments, derived from filamentous fungi Aspergillus genus, being useful for manufacturing a protein. One of the DNA sequences or their branches an effectively activate transcription of a gene encoding a target protein irrespective of the presence or absence of glucose. The DNA sequences and their fargments can constantly activate gene transcription. This polymucleotide sequence represents one of the 74 filamentous fungi Aspergillus genus DNA sequences of the invention.

Sequence 538 BP; 128 A; 123 C; 132 G; 155 T; 0 U; 0 Other;

DB 9; Length 538; 2; Indels le+02; Score 16.8; DE Pred. No. 1e+020; Mismatches 20 1 CTGGACAGGTTAGGGCTTTG 84.0%; Conservative Local Similarity es 18; Conser Query Match Best Loc Matches 셤 ઢ

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Gaps

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494 CIGGACAGGIIGGGGIIIIG 475

RESULT 8 ABZ56309/

ABZ56309 standard; cDNA; 589

ABZ56309;

ВЪ.

28-MAR-2003 (first entry)

Aspergillus oryzae polymucleotide SEQ ID NO 5422

Aspergillus oryzae; fermentation; fungus; industrial; BST; expressed sequence tag; gene; ss.

Aspergillus oryzae

WO200279476-A1.

10-OCT-2002

22-MAR-2002; 2002WO-IB000890.

30-MAR-2001; 2001JP-00098371.

NAT INST ADVANCED IND SCI & TECHNOLOGY.
NAT RES INST BREWING.
NAT FOOD RES INST MIN AGRIC. (NAAD-) N (NARE-) N (NORQ) N

Horiuchi I Abe K; Akita O, Kashiwagi Y, Kitamoto K, Kobayashi T, Kitamoto N, Gomi K, Machida M, Takeuchi M,

WPI; 2003-046817/04.

Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes.

Claim 1; SEQ ID NO 5422; 48pp + Sequence Listing; Japanese

The invention relates to a polynucleotide having any of 6006 specific sequences (ABSC6898-ABSE6893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, olid, early germination, alkaline, high temperature, low temperature or maltose ulture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryvae; Trichoderma resesi; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss. Gaps ő Length 589; Sequence 589 BP; 143 A; 210 C; 95 G; 141 T; 0 U; 0 Other; Indels Multiple gene expression; filamentous fungal cell; EST; Score 16.8; DB 7; Pred. No. 1e+02; 0; Mismatches 2; at ftp.wipo.int/pub/published_pct_sequences Aspergillus oryzae EST SEQ ID NO:7054. (NOVO) NOVO NORDISK BIOTECH INC. (NOVO) NOVO NORDISK AS. 1 CTGGACAGGTTAGGGCTTTG 20 100 creckchegerreeserrres 81 ° ВР 84.0%; 90.0%; AAF14531 standard; cDNA; 809 22-MAR-2000; 2000WO-US007781. (first entry) Local Similarity 90.0 es 18; Conservative Aspergillus oryzae WO200056762-A2. 22-MAR-1999; 13-MAR-2001 28-SEP-2000 AAF14531; Quefy Match Best Loca Matches RESULT 9 AAF14531/ 8 X G ઠે 셤

Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags. WPI; 2000-594572/56

Olsen PB;

Clausen IG,

Shuster JR, Kauppinen S,

Berka RM, Rey MW,

Claim 88; Page 2863-2864; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of genes in a first filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes con a first filamentous fungal (FF) cell relative to expression of genes in a first filamentous fungal (FF) cell relative to expression of the expression of genes from FF cells allows the production potential cof the microorganisms to be improved. New genes may be discovered, one spible functions of unknown open reading frames can be identified and copen number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, cor catabolic pathway engineering. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, products to facilitate analysis of the results. AAF01478 to AAF11847 coppered to ESTS from ABPERSILES TOW ESTS from

Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;

26-DEC-2001; 2001US-00035832. 26-DEC-2002; 2002WO-US041414.

WO2003057146-A2

gene; ds.

17-JUL-2003

Human DAD1 carcinoma associated gene, SEQ ID NO:1478.

(first entry)

06-NOV-2003

ADA02960;

ADA02960 standard; DNA; 44325 BP

ADA02960,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from
Trichoderma reesei, which are all specifically claimed in the present
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                 Match 84.0%; Score 16.8; DB 3; Length 809; Local Similarity 90.0%; Pred. No. 1.1e+02; es 18; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2305 BP; 457 A; 730 C; 621 G; 497 T; 0 U; 0 Other;
                                                                  Sequence 809 BP; 182 A; 265 C; 161 G; 199 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 795; 205pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Human coding sequence, SEQ ID 795
                                                                                                                                                                                                                                                                                             ADA53227 standard; cDNA; 2305 BP.
                                                                                                                                                                       1 CTGGACAGGTTAGGGCTTTG 20
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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24-JAN-2002; 2002US-0350435P.
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Best Local Similarity 90.0%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003 (first entry)
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P-PSDB; ADA54866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Yamamoto J,
                                  invention
                                                                                                                                                                                                                                                                                                                              ADA53227;
                                                                                                                                                                                                        62
                                                                                                   Query Match
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a blochip comprising CA nucleic acid, or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism or a random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protoncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44325 BP; 11218 A; 9675 C; 9902 G; 13530 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 84.0%; Score 16.8; DB 8; Length 44225; Best Local Similarity 90.0%; Pred. No. 1.5e+02; Aatches 18; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1478; 245pp; English.
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ADB72698 standard; DNA; 44325 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-587068/55
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1 CTGGACAGGTTAGGGCTTTG 20

us-09-939-853a-140.rng

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                              New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                     The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinomassociated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                         Sequence 44325 BP; 11218 A; 9675 C; 9902 G; 13530 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, ds, gene; pain, neuronal tissue; gene therapy;
spinal segmental nerve injury, chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 16.8; DB 9; Length 44325; 90.0%; Pred. No. 1.5e+02; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Costigan M;
                                                                                                                                                                                         Claim 1; SEQ ID NO 226; 983pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   38075 CTGGACAGGATAGGGCTGTG 38056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene U72649, SEQ ID NO 3762
                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADES7896 standard; DNA; 2446 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGGACAGGTTAGGGCTTTG
               30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                          Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                             (SAGR-) SAGRES DISCOVERY
                                                                                                     WPI; 2003-513603/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D'urso D,
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GENBANK; U72649.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                       Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE57896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woolf C,
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ADE57896
   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                    human; d8; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44325 BP; 11218 A; 9675 C; 9902 G; 13530 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 84.0%; Score 16.8; DB 9; Length 44325; Best Local Similarity 90.0%; Pred. No. 1.5e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 526; 2304pp; English.
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00937722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                    26-DEC-2001; 2001WO-US051291
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                            04-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                    Engelhard EK;
                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-239337/23
                                                                                                                                                            WO2003008583-A2.
                                                      Human DAD1 gene
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                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                    Morris DW,
ADB72698
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or human polymucleotides or application to the mucleic acid sequence. Also caliente restriction of the nucleic acid sequence. Also comprising the vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, amethod for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a subjected to pain and a subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity of one or more of the polymucleotides of the compound that method for identifying a compound or small molecule that regulates the activity of one or more of the polympetides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polympetides or their antibodies. The polymucleotides or their activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CUI) and spared nerve injury (CUI) and spared nerve injury (CUI) and spared nerve injury (Mul) and spared nerve injury (Mul) in an animal expense of the polympetides of the invention which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was for this patent did not form part of the printed specification, but were the sequence of the polympetides of the invention of the polympetides prove the sequence of the polympetides of the invention of the polympetides of the invention of the polympetides of
       composition comprising two or more isolated rat
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ô Score 16.4; DB 9; Length 2446; Pred. No. 1.9e+02; 0; Mismatches 1; Indels 0; Sequence 2446 BP; 567 A; 637 C; 596 G; 646 T; 0 U; 0 Other; / Match 82.0%; Local Similarity 94.4%; Les 17; Conservative (Query Match Best Loca Matches

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1850 GGACAGGCTAGGGCTTTG 1867 3 GGACAGGTTAGGGCTTTG 20 ò 셤

ADES7892 standard; DNA; 2446 BP RESULT 15

ADE57892;

29-JAN-2004 (first entry)

Human gene U72649, SEQ ID NO 3758

Human, ds, gene, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury, SNI, Chung.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

Costigan M; Befort K, Woolf C, D'urso D,

WPI; 2003-268312/26. GENBANK; U72649.

WO2003016475-A2. Homo sapiens. 27-FEB-2003

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, and entrievive or allelic variation'of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a chat is differentially expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that manimal of one or meal molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating control of the invention of pain and a pharmaceutical composition comprising the one or more of the compound that modulates its activity is useful for preparing a medicament for treating collypeptides or their antibodies. The polypeptides of the invention injury (CCI) and spared nerve injury (SM1) in an animal (e.g. spiral segmental nerve injury (SM1) in an animal (e.g. specification) which encodes one of the polypeptides of the invention of the raph, but has patent did not form part of the polypeptides of the invention of the value of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of the publication of New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal. Sequence 2446 BP; 567 A; 637 C; 596 G; 646 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences. Claim 1; Page; 1017pp; English.

ö 82.0%; Score 16.4; DB 9; Length 2446; 94.4%; Pred. No. 1.9e+02; ive 0; Mismatches 1; Indels 0; 17; Conservative Query Match Best Local Similarity Matches 17; Conserv tches

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1850 GGACAGGCTAGGGCTTTG 1867 3 GGACAGGTTAGGGCTTTG 20 ઠે

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Mammalia, Butheria,
1 (bases 1 to 986)
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Homo sapiens
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BQ054265/c
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VERSION
KEYWORDS
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ORGANISM
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BQ053486/c
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AUTHORS
TITLE
JOURNAL
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                                                                            /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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MIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_91"
/note="Grgan: prostate, Vector: pCMV-SPORT6; Site_1: Not Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Faraday Avenue Genoscope sequence ID : CSODJ013BF05QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 13; Length 616; 100.0%; Pred. No. 88; tive 0; Mismatches 0; Indels (
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                                                             'organism="Homo sapiens"
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Location/Qualifiers
1, 778
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/db_xref="taxon:9606"
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BG178487.1 GI:12685190
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Homo sapiens
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DEFINITION
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KEYWORDS
                     FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="uaxon:9606"
/db_xref="uaxon:9606"
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/lab_hofe="DH10B (phage-resistant)"
/clone lib="WHH MGC 106"
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/clone lib="WHH MGC 106"
/note="Corgan: blood; Vector: poTB7; Site_1: xhoI; Site_2:
/clone lib="Amade by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
/gcAcGAGGG: Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript I RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           986 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6830248 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936339
BQ054265
BQ053486 879 bp mRNA linear EST 29-MAR-2002
AGENCOURT 6822017 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935253
5, mRNA sequence.
BQ053486
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I (Dases I to 878)

IH-MGC Http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Daniel McVicar, DBS/NCI

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Phttp://image.llnl.gov

High quality sequence stop: 394.
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Contact: Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
BRail: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9825.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODE005AF12QP1&cluster=9825.r. Contact:
Feng Liang Enail: fliang@lifetech.com URL:
http://tulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE005AF12QP1.
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/note="Organ: bIood; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: bIood; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: bIood; Vector: pOTB7; Site_1: XhoI; Site_2:
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ALS41041 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE005YK23
ALS41041
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/close lib="Homo sapiens PLACENTA"

/clone lib="Wector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched;
with a NotI-oligo(dT) primer. Five prime end enriched;
with a NotI and clone was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Thi,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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100.0%; Score 20; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels (
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ilarity 100.0%; Pred. No. 95;
Conservative 0; Mismatches
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|db_xref="taxon:9606"
|clone="CS0DE005YK23"
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AUTHORS
TITLE
JOURNAL
COMMENT
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIM #006_106"
/note="Organ: bLood; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
into BCORI/KhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT 6830234 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5936362
57, mRNA sequence.
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1 (bases 1 to 1020)

NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                        Conscion Accurement: Dr. Daniel McVicar, DBS/NCI
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CONA Library Preparation: Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2125 row: i column: 12
High quality sequence stop: 515.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2125 row: j column: 11
High quality sequence stop: 556.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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/clone="IMAGE:5936339"
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BQ054281.1 GI:19813621
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Kenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:8355"
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          GF:27520161
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                                                                                                                                              BU327205 901 bp mRNA linear EST 28-NOV-2002 603490679F1 CSEQCHN63 Gallus gallus cDNA clone ChEST392m20 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 901)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T. Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Pred. No. Se+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
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/mol_twin="White Leghorn, Hisex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dev_stage="36"
lab_host="DH10B"
CTGGACAGGTTAGGGCTTTG 343
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Gallus gallus
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Matches 19; Conservative
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FEATURES

MEDLINE PUBMED COMMENT

TITLE JOURNAL

REFERENCE AUTHORS

RESULT 8 CA987486/c

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ORIGIN

DEFINITION

ACCESSION

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Martha Rebbert, Steven L. Klein, Ph.D.

Tissue Produrement: Martha Rebbert, Steven L. Klein, Ph.D.

Tissue Produrement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI4444 row: g column: 24

High quality sequence start: 228

High quality sequence start: 228

High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo" (stage 10) "
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/clone lib="NH1DB XGC Embl"
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/note="Vector: pcNv-SPORT6; Site_1: NotI; Site_2: SalI;
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/note="vector: pcNv-SPORT6; Site_1: NotI; Site_2: SalI;
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/note="vector: pcNv-SPORT6; Site_1: NotI; Site_1: Note: This site a Xenopus Gene Collection (XGC) library."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (basea 1 to 332) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Homos apprend; Butheria; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)
1 (bases 1 to 413)
2 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.

1 Macholished (2003)
2 Contact: Ina Rolfs

RZPD Deutsches Resourcenzentrum fuer Genomforschung GmbH
IM Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAG998P23333.

RZPD; IMAG998P233333.

RZPDIIB; I.M.A.G.E. CONA Clone Collection; Human Unigeneset - RZPD3 (RZPDIIB NO.972)
http://www.rzpd.de/CloneCards/Cgi-bin/showiib.p.) pl. cgi/response?lib/No=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Fax: +49 30 32639 101
       BX089099 Soares_testis_NHT Homo Bapiens cDNA clone IMAGD998P233333 ; IMAGE:1322374, mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Scares testis_NHT"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker, Site_1: Not I; Site_2: Eco RI; Ist strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 9; Length 357;
Pred. No. 1.2e+03;
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/lab host="DH10B"
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BX089099.1 GI:27823687
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BX089099
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KEYWORDS
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Email: cgapbs-r@mail.nih.gov

EDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

EDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

EDNA Library Arrayed by: Greg Lennon, Ph.D.

EDNA Library Arrayed by: Greg Lennon, Ph.D.

EDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-GAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 466 Std Error: 0.00

Seq primer: --40mil Error: Amersham.
                                                                                                                                                                                                                                                                    /clone_lib="Scares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l Not I, Site_2: Eco RI, 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(GT)
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA759254 357 bp mRNA linear EST 29-DEC-1998
ah84912.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2008) 1 to 357)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lab host="DH10B"
/clone_lib="Soares_testis_NHT"
/note="Vector: pT773D-Pac"(Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 17.4; DB 9; Length 332; ilarity 94.7%; Pred. No. 1.2e+03; Conservative 0; Mismatches 1; Indels c
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 472 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 316.
Location/Qualifiers
                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1292678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1322374"
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                                                                                                                                                                                                                                                   lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 CTGGACAGGTCAGGGCTTT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGACAGGTTAGGGCTTT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA759254.1 GI:2807117
                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                        primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                   source
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AA759254/c
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212 bp mRNA linear EST 01-APR-2003 cDNA, mRNA sequence.
CB487227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
                                                                                                                              Landrowicz, B. J. Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Farddle, C.J., Gupta, A., Hansen, M., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Max, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, T., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T., Vogel, P., Walke, W., Xu, N., Walk Kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP OmniBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Buteleostei;
Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus.
1 (Dases i to 212)
1 (Bass Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.
                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 177)
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Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A survey of Salmo salar transcripts from high complexity cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO BOX 3020 STM CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="0ST246195"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.8; DB 29;
Pred. No. 2.1e+03;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/EV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: Gene Trap.
Location/Qualifiers
                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGGACAGGTTAGGGCTTTG 20
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Best Local Similarity 90.0
Matches 18; Conservative
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CB487227/c
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Totofi,Y., Watanabe,H. and Sakaki,Y.
Totofi,Y., Watanabe,H. and Sakaki,Y.
Totofi,Y., Watanabe,H. and Sakaki,Y.
Totofi,Y., Watanabe,H. and Sakaki,Y.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-xu, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:s1-45-503-911, Pax:81-45-503-9170)
Tel:s1-45-503-911, Pax:81-45-503-9170)
Was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                            GSS 02-NOV-2001
                                                                                                                                                                                                                                                                                                              AG048198 740 bp DNA linear GSS 02-NCV-200
Pan troglodytes DNA, clone: PTB-027P05.R, genomic survey sequence.
AG048198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
    by Bento Soares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuijyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                          Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                     87.0%; Score 17.4; DB 13;
94.7%; Pred. No. 1.3e+03;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .740
/organism="Pan troglodytes"
/organism="renomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector : pxs145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (chimpanzee)
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                                                                                              Local Similarity
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                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                          GSS.
                                                                       Query Match
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Gaps

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Length 177;